

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 18, 2002, 10:33:53 ; Search time 13 Seconds  
(without alignments)  
319.412 Million cell updates/sec

Title: US-09-218-913D-52

Perfect score: 948

Sequence: 1 ADRESIHDFCLVSKVVGRC.....ACMLRCFRQENPLPLGSK 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	948	100.0	252	1	US-08-685-660A-7
2	948	100.0	252	2	US-08-974-196-7
3	948	100.0	252	4	US-09-071-709-10
4	948	100.0	252	4	US-09-013-896A-2
5	312	32.9	513	4	US-08-685-558A-18
6	299.5	31.6	348	4	US-09-071-709-2
7	297	31.3	51	4	US-09-013-896A-10
8	297	31.3	51	4	US-09-013-896A-11
9	247.5	26.1	122	2	US-08-422-333-12
10	247.5	26.1	122	6	5187153-20
11	247.5	26.1	122	6	5220013-23
12	244.5	25.8	143	2	US-08-422-333-10
13	244.5	25.8	143	6	5223482-20
14	244.5	25.8	144	6	5187153-18
15	244.5	25.8	147	1	US-08-358-160-72
16	243.5	25.7	127	6	5466783-21
17	241.5	25.5	123	6	5466783-21
18	233.5	24.6	122	6	5223482-22
19	233.5	24.6	276	1	US-07-828-920A-1
20	233.5	24.6	276	1	US-08-437-841-9
21	233.5	24.6	276	1	US-08-286-521-9
22	233.5	24.6	276	1	US-08-436-175-9
23	233.5	24.6	276	2	US-08-796-850-1
24	233.5	24.6	276	3	US-08-854-764-3
25	233.5	24.6	276	4	US-08-943-682-9
26	233.5	24.6	276	5	PCT-US95-09377-3
27	233.5	24.6	276	5	PCT-US95-09464-9

28	233.5	24.6	277	1	US-07-844-297-1	Sequence 1, Appli
29	233.5	24.6	304	1	US-08-026-145-2	Sequence 2, Appli
30	233.5	24.6	304	1	US-08-446-646-9	Sequence 9, Appli
31	233.5	24.6	304	1	US-08-676-125A-18	Sequence 18, Appli
32	233.5	24.6	304	2	US-09-136-012A-18	Sequence 18, Appli
33	233.5	24.6	304	3	US-08-676-124-1	Sequence 1, Appli
34	233.5	24.6	304	3	US-08-208-264A-25	Sequence 25, Appli
35	233.5	24.6	304	3	US-09-414-878-1	Sequence 1, Appli
36	233.5	24.6	304	3	US-09-240-136-1	Sequence 2, Appli
37	233.5	24.6	304	4	US-09-054-782-2	Sequence 2, Appli
38	233.5	24.6	304	4	US-09-421-097-25	Sequence 25, Appli
39	233.5	24.6	304	6	5466783-2	Patent No. 5466783
40	233.5	24.6	352	3	US-08-854-764-2	Sequence 2, Appli
41	233.5	24.6	352	5	PCT-US95-09377-2	Sequence 2, Appli
42	232.5	24.5	123	6	5466783-22	Patent No. 5466783
43	232	24.5	161	1	US-08-437-841-19	Sequence 19, Appli
44	232	24.5	161	1	US-08-286-521-19	Sequence 19, Appli
45	232	24.5	161	1	US-08-436-175-19	Sequence 19, Appli

## ALIGNMENTS

RESULT 1  
US-08-685-660A-7  
; Sequence 7, Application US/08685660A  
; Patent No. 5731412  
; GENERAL INFORMATION:  
; APPLICANT: SHIMOMURA, Takeshi  
; APPLICANT: KAWAGUCHI, Toshiya  
; APPLICANT: KITAMURA, Naomi  
; TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME  
; TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
; STREET: 2100 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/685,660A  
; FILING DATE: 24-JUL-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JPA Hei 7-187134  
; FILING DATE: 24-JUL-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KIT, Gordon  
; REGISTRATION NUMBER: 30,764  
; REFERENCE/DOCKET NUMBER: Q-42295  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 293-7060  
; TELEFAX: (202) 293-7860  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 252 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-685-660A-7

Query Match 100.0%; Score 948; DB 1; Length 252;  
Best Local Similarity 100.0%; Pred. No. 3.1e-92;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 ADRESIHDFCLVSKVVGRCASMPRWNYVTGSCQLFVYVGCDGNSNNYTKKECLKK 60  
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Db 28 ADERSIHDCLVSKVGRASMPRWYNTDGSQCLFVYGGDGNNSNYLTKEECLKK 87  
Qy 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEHSDMFNVEEYCTANAVTGPCRASFP 120  
Db 88 CATVTENATGDLATSRNAADSSVPSAPRRQDSEHSDMFNVEEYCTANAVTGPCRASFP 147  
Qy 121 RWFYDVERNSCNFIYGGCRGNKNSYRSEAEACMLRCFRQENPPLPLGSK 170  
Db 148 RWFYDVERNSCNFIYGGCRGNKNSYRSEAEACMLRCFRQENPPLPLGSK 197

RESULT 2  
US-08-974-196-7  
; Sequence 7, Application US/08974196  
; Patent No. 5854396  
; GENERAL INFORMATION:  
; APPLICANT: SHIMOMURA, Takeshi  
; APPLICANT: KAWAGUCHI, Toshiya  
; APPLICANT: KITAMURA, Naomi  
; TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME  
; TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
; STREET: 2100 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20037

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,196  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/685,660  
; FILING DATE: 24-JUL-1996  
; APPLICATION NUMBER: JPA Hei 7-187134  
; FILING DATE: 24-JUL-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KIT, Gordon  
; REGISTRATION NUMBER: 30,764  
; REFERENCE/DOCKET NUMBER: Q-42295  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 293-7060  
; TELEFAX: (202) 293-7860  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 252 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-974-196-7

Query Match 100.0%; Score 948; DB 2; Length 252;  
Best Local Similarity 100.0%; Pred. No. 3.1e-92;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADERSIHDCLVSKVGRASMPRWYNTDGSQCLFVYGGDGNNSNYLTKEECLKK 60  
Db 28 ADERSIHDCLVSKVGRASMPRWYNTDGSQCLFVYGGDGNNSNYLTKEECLKK 87  
Qy 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEHSDMFNVEEYCTANAVTGPCRASFP 120  
Db 88 CATVTENATGDLATSRNAADSSVPSAPRRQDSEHSDMFNVEEYCTANAVTGPCRASFP 147  
Qy 121 RWFYDVERNSCNFIYGGCRGNKNSYRSEAEACMLRCFRQENPPLPLGSK 170  
Db 148 RWFYDVERNSCNFIYGGCRGNKNSYRSEAEACMLRCFRQENPPLPLGSK 197

RESULT 3  
US-09-071-709-10  
; Sequence 10, Application US/09071709  
; Patent No. 6171790  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Lal, Preeti  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Patterson, Chandra  
; TITLE OF INVENTION: HUMAN PROTEASE ASSOCIATED PROTEINS  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/071,709  
; FILING DATE: Filed Herewith  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CERRONE, MICHAEL C.  
; REGISTRATION NUMBER: 39,132  
; REFERENCE/DOCKET NUMBER: PF-0513 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 252 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-071-709-10

Query Match 100.0%; Score 948; DB 4; Length 252;  
Best Local Similarity 100.0%; Pred. No. 3.1e-92;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADERSIHDCLVSKVGRASMPRWYNTDGSQCLFVYGGDGNNSNYLTKEECLKK 60  
Db 28 ADERSIHDCLVSKVGRASMPRWYNTDGSQCLFVYGGDGNNSNYLTKEECLKK 87  
Qy 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEHSDMFNVEEYCTANAVTGPCRASFP 120  
Db 88 CATVTENATGDLATSRNAADSSVPSAPRRQDSEHSDMFNVEEYCTANAVTGPCRASFP 147  
Qy 121 RWFYDVERNSCNFIYGGCRGNKNSYRSEAEACMLRCFRQENPPLPLGSK 170  
Db 148 RWFYDVERNSCNFIYGGCRGNKNSYRSEAEACMLRCFRQENPPLPLGSK 197

RESULT 4  
US-09-013-896A-2  
; Sequence 2, Application US/09013896A  
; Patent No. 6262233  
; GENERAL INFORMATION:  
; APPLICANT: GENTZ, REINER  
; TITLE OF INVENTION: TISSUE FACTOR PATHWAY INHIBITOR-3  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVE., NW, STE. 600

```

; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/013,896A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1290001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 252 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-013-896A-2

Query Match 100.0%; Score 948; DB 4; Length 252;
Best Local Similarity 100.0%; Pred. No. 3.1e-92;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADERSIHDFCLVSKVVGRCRASPRWYNTDSCQLFYVGGCDGNSNNLTKEECLKK 60
Db 28 ADERSIHDFCLVSKVVGRCRASPRWYNTDSCQLFYVGGCDGNSNNLTKEECLKK 87

QY 61 CATVTENATGDLATSNADSSVPSAPRRQDSHSDMFNVEEYCTANAVTGPCRASFP 120
Db 88 CATVTENATGDLATSNADSSVPSAPRRQDSHSDMFNVEEYCTANAVTGPCRASFP 147

QY 121 RWYFDVERNSCNFFIYGGCGNKNYSRSEACMLRCFROQENPLPLGSK 170
Db 148 RWYFDVERNSCNFFIYGGCGNKNYSRSEACMLRCFROQENPLPLGSK 197

RESULT 5
US-08-685-558A-18
; Sequence 18, Application US/08685558A
; Patent No. 6225081
; GENERAL INFORMATION:
; APPLICANT: SHIMOMURA, Takeshi
; APPLICANT: KAWAGUCHI, Toshiya
; APPLICANT: KITAMURA, Naomi
; APPLICANT: MIYAZAWA, Keiji
; TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,558A
; FILING DATE: 24-JUL-1996
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: JPA Hei 7-187135
; FILING DATE: 24-JUL-1995
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 513 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; STRAIN: MKN45
; US-08-685-558A-18

Query Match 32.9%; Score 312; DB 4; Length 513;
Best Local Similarity 33.5%; Pred. No. 7.6e-25;
Matches 67; Conservative 24; Mismatches 71; Indels 38; Gaps 5;

QY 5 RSIHDFCLVSKVVGRCRASPRWYNTDSCQLFYVGGCDGNSNNLTKEECLKKCATV 64
Db 244 KOTEDYCLASNKVGRGSGSFPWYDPTQICKSFYVGGCLGNKNYLREEECILACRGV 303

QY 65 -----TENATGDLATSNADSSVPSAPRRQDSHSDMFNVEEYCTANAVTGPCRASFP 102
Db 304 QGFSMERHHPVCSGTQPTQFRGSCNGCCIDSLFLECDTTPNCPPDASDEAAACEKYTSGFDEL 363

QY 103 EE-----YCTANAVTGPCRASFPWYFDVERNSCNFFIYGGCGNKNYSRSEACML 154
Db 364 QRHFFSDKGHCVDLPTDGLCKESIPRWYINPFSEHCAREFTYGGCYGNKNNFEEQOOLE 423

QY 155 RC-----FRQENPLPLP 166
Db 424 SCRGISKDVFGLRREIP 443

RESULT 6
US-09-071-709-2
; Sequence 2, Application US/09071709
; Patent No. 6171790
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Tang, Y. Tom
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Patterson, Chandra
; TITLE OF INVENTION: HUMAN PROTEASE ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,709
; FILING DATE: Filed Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0513 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 348 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BLADNOT04
; CLONE: 1319265
US-09-071-709-2

Query Match 31.6%; Score 299.5; DB 4; Length 348;
Best Local Similarity 31.2%; Pred. No. 9.6e-24;
Matches 69; Conservative 24; Mismatches 65; Indels 63; Gaps 7;

QY 5 RSTHDFCLSVKVVYGR-CRASMPRWYNTDGSQCLFYGGCGNSNNYLTKECLKKCAT 63
Db 62 KQTEYCLASNKVGRRCRGSFPRWYDPTQICKSFYGGCLGNKNYLRREECILACRG 121
QY 64 VTNATGDLATRNAADSSVPSAP---RRQ-----DSED-- 94
Db 122 V----QGGPLRGSSGAATPPQGSMEHRHPVCSGTQPTQFRCSNGCCIDSPLECDTTP 177
QY 95 ---HSSDMFNVEY-----CTANAVTGPCRASFPRWYFDVERNSCNN 133
Db 178 NCPDASDEAAACEYTSGFDELQRIHPFSDKGHCVDLPDTGLCKESTPRWYINPFSEHCAR 237
QY 134 FIYGGCGNKNNSRSEACMLRC-----FRQENPPLP 166
Db 238 FTYGGCGNKNNEEQCLSCRGISKRDVGLRREIPI 278

RESULT 7
US-09-013-896A-10
; Sequence 10, Application US/09013896A
; Patent No. 6262233
; GENERAL INFORMATION:
; APPLICANT: GENTZ, REINER
; TITLE OF INVENTION: TISSUE FACTOR PATHWAY INHIBITOR-3
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, STE. 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/013,896A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1290001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-013-896A-10

Query Match 31.3%; Score 297; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.5e-24;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 CTANAVTGPCRASFPRWYFDVERNSCNNFIYGGCGNKNNSRSEACMLRC 156
Db 1 CTANAVTGPCRASFPRWYFDVERNSCNNFIYGGCGNKNNSRSEACMLRC 51

RESULT 9
US-08-422-333-12
; Sequence 12, Application US/08422333
; Patent No. 5912410
; GENERAL INFORMATION:
; APPLICANT: CORDELL, Barbara L.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL DISPLAYING
; THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scios, Inc.
; STREET: 2450 Bayshore Parkway
; CITY: Mountain View
; STATE: CA
; COUNTRY: USA
; ZIP: 94043
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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QY 11 CLVSKVVGRCRASMPRWYNTDGSQCLFYGGCGNSNNYLTKECLKKC 61
Db 1 CLVSKVVGRCRASMPRWYNTDGSQCLFYGGCGNSNNYLTKECLKKC 51

RESULT 8
US-09-013-896A-11
; Sequence 11, Application US/09013896A
; Patent No. 6262233
; GENERAL INFORMATION:
; APPLICANT: GENTZ, REINER
; TITLE OF INVENTION: TISSUE FACTOR PATHWAY INHIBITOR-3
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, STE. 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/013,896A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1290001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-013-896A-11

Query Match 31.3%; Score 297; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.5e-24;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 CTANAVTGPCRASFPRWYFDVERNSCNNFIYGGCGNKNNSRSEACMLRC 156
Db 1 CTANAVTGPCRASFPRWYFDVERNSCNNFIYGGCGNKNNSRSEACMLRC 51

RESULT 9
US-08-422-333-12
; Sequence 12, Application US/08422333
; Patent No. 5912410
; GENERAL INFORMATION:
; APPLICANT: CORDELL, Barbara L.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL DISPLAYING
; THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scios, Inc.
; STREET: 2450 Bayshore Parkway
; CITY: Mountain View
; STATE: CA
; COUNTRY: USA
; ZIP: 94043
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

Qy	69	TGDLATSRNAADSVSPAPRRQSDHSSDMFNYEEYCTANAVTGPCRASFPFRWYFDVER	120
Db	59	-----EACNLPIVQGPCRAFIQLWAFAVAK	83
Qy	129	NSCNFTIYGCGRGNKNSYRSEECMLRC	156
Db	84	GKCVRFSYGGCKGNKNFYSQKEKEYC	111
RESULT 11			
5220013-23			
; Patent No. 5220013			
; APPLICANT: PONTE, PHYLLIS A.;CORDELL, BARBARA			
; TITLE OF INVENTION: DNA SEQUENCE USEFUL FOR THE DETECTION			
; OF ALZHEIMER'S DISEASE			
; NUMBER OF SEQUENCES: 30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/07/444,118			
; FILING DATE: 30-NOV-1989			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: 87,002			
; FILING DATE: 18-AUG-1987			
; APPLICATION NUMBER: 8,810			
; FILING DATE: 30-JAN-1987			
; APPLICATION NUMBER: 948,376			
; FILING DATE: 31-DEC-1986			
; APPLICATION NUMBER: 932,193			
; FILING DATE: 17-NOV-1986			
; SEQ ID NO:23;			
; LENGTH: 122			
5220013-23			
Query Match	26.1%;	Score 247.5; DB 6; Length 122;	
Best Local Similarity	32.4%;	Pred. No. 7.5e-19;	
Matches	48; Conservative	16; Mismatches	45; Indels 39; Gaps
Qy	9	DFCLVSKVGRCRASMPRWYNVTGSCQLFVYGGCDGHSNNYLTFEECLKKCAIVTENA	68
Db	3	DSOLDYSQGPCLGLPKRFYNGTSMACETFLYGGCMGNLNNPLSOKELQTCRTV----	58
Qy	69	TGDLATSRNAADSVSPAPRRQSDHSSDMFNYEEYCTANAVTGPCRASFPFRWYFDVER	128
Db	59	-----EACNLPIVQGPCRAFIQLWAFAVAK	83
Qy	129	NSCNFTIYGCGRGNKNSYRSEECMLRC	156
Db	84	GKCVRFSYGGCKGNKNFYSQKEKEYC	111
RESULT 12			
US-08-422-333-10			
; Sequence 10, Application US/08422333			
; Patent No. 5912410			
; GENERAL INFORMATION:			
; APPLICANT: CORDELL, Barbara L.			
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL DISPLAYING			
; TITLE OF INVENTION: THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S DIS			
; NUMBER OF SEQUENCES: 30			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Scios, Inc.			
; STREET: 2450 Bayshore Parkway			
; CITY: Mountain View			
; STATE: CA			
; COUNTRY: USA			
; ZIP: 94043			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/422,333			

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Db      105 GKCVLFYGGCGNGNKFSEKCECREYC 132
| | | | | | | | | | | | | | | | | |
RESULT 14
5187153-18
; Patent No. 5187153
; APPLICANT : CORDELL, BARBARA; SCHILLING, JAMES W.; KATUNUMA, NOBUHIKO
; TITLE OF INVENTION: METHODS OF TREATMENT USING ALZHEIMER'S
; AMYLOID POLYPEPTIDE DERIVATIVES
; NUMBER OF SEQUENCES: 33
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/502,273
; FILING DATE: 29-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 361,912
; FILING DATE: 06-JUN-1989
; APPLICATION NUMBER: 359,911
; FILING DATE: 12-MAY-1989
; APPLICATION NUMBER: 87,002
; FILING DATE: 18-AUG-1987
; APPLICATION NUMBER: 8,810
; FILING DATE: 30-JAN-1987
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193
; FILING DATE: 17-NOV-1986
; SEQ ID NO: 18:
; LENGTH: 144
5187153-18

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	Matches	47	Conservative	15	Mismatches	47	Indels	39	Gaps
QY	9	DFLVSKVVGRCRASPRWRYNTDGSQCLFVYGDDGNSNNYLTKKECLKKCATATENA	68						
Db	24	DSOQLGYSAGPCMGMTSRFYNGTSMACETFYQGGCMGNFNVEKECLQTCTRVAA--	81						
QY	69	TGDLATSRNAADSVPSAPRRQSDHSSDMFNYEEYCTANAVTGPCRSFPFWYFDVER	128						
Db	82	-----CNLPVIRGPCRAFIQLWAFDAVK	104						
QY	129	NSCNFFTYGCRGNKNYSRSEAEAMCRC	156						
Db	*105	GKCVLFPYGCOCGNKNFYSEKKCREYC	132						

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1  TITLE OF INVENTION:  ENGINEERED HUMAN-DERIVED KUNITZ
2  TITLE OF INVENTION:  DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
3  NUMBER OF SEQUENCES:  234
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE:  BROWDY AND NEIMARK
6  STREET:  419 Seventh Street, N.W. Suite 300
7  CITY:  Washington
8  STATE:  District of Columbia
9  COUNTRY:  USA
10 ZIP:  20004
11 COMPUTER READABLE FORM:
12 MEDIUM TYPE:  Floppy disk
13 COMPUTER:  IBM PC compatible
14 OPERATING SYSTEM:  PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 147 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-72

Query Match 25.8%; Score 244.5; DB 1; Length 147;
Best Local Similarity 32.4%; Pred. No. 2e-18;
Matches 48; Conservative 14; Mismatches 47; Indels 39; Gaps 1;

QY 9 DFCLVSKVYGRCPASMPRWYNYVTDGSCQLFVYGGCDGNSNNYLTKECLKKCATVTENA 68
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
24 DSCOLGYSAGPCMGWTSRYFYNGTSMACETFYGGCMGNGNNFVTEKECLQTCRTVAA-- 81

QY 69 TGDLATSRNAADSSVPSAPRRQDSEHDSSDMFNYEYCTANAVTGPCRASFPFWYFDVER 128
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
82 -----CNLPYVRGPCRAFIQLWAFDAVK 104

QY 129 NSCNNFYGGCGNKNYSRSEACMLRC 156
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
105 GKCVLFPGYGGCGNGNKNFYSEKECREYC 132

Search completed: October 18, 2002, 10:36:06
Job time : 15 secs
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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 18, 2002, 10:33:48 ; Search time 28 Seconds  
(without alignments)  
1050.326 Million cell updates/sec

Title: US-09-218-913d-52  
Perfect score: 948  
Sequence: 1 ADERSIHDFCLVSKVGRG.....ACMLRCFRQENPPLGLSK 170

Scoring table: BLOSUM62  
Gap 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_19.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	948	100.0	252	4	Q969E0
2	381	40.2	195	11	Q9D808
3	294	31.0	507	11	Q9D3K4
4	294	31.0	507	11	Q99J04
5	259	27.3	3060	5	Q9VAV4
6	256.5	27.1	1572	5	Q44938
7	255	26.9	3198	5	Q9U8G8
8	252	26.6	287	13	Q93424
9	250.5	26.4	2167	5	Q76840
10	250	26.4	2174	5	Q9QGR0
11	244.5	25.8	151	4	P78491
12	240	25.3	2225	5	O45881
13	239.5	25.3	396	6	Q28874
14	235.5	24.8	349	11	Q9DBJ9
15	235.5	24.8	349	11	Q925W1
16	233.5	24.6	352	11	O70160

17	228	24.1	251	4	O95103	O95103 homo sapien
18	227.5	24.0	246	11	Q9Z208	Q9Z208 mus musculus
19	222	23.4	1043	5	O17644	O17644 caenorhabdi
20	219.5	23.2	342	13	P70004	P70004 xenopus lae
21	219	23.1	922	5	Q21418	Q21418 caenorhabdi
22	209	22.0	1743	5	Q9XWX5	Q9XWX5 caenorhabdi
23	208	21.9	751	11	Q60709	Q60709 mus musculus
24	208	21.9	763	11	O61482	O61482 mus musculus
25	200	21.1	523	4	O14594	O14594 homo sapien
26	200	21.1	1599	5	Q09983	Q09983 caenorhabdi
27	199	21.0	1522	5	Q22685	Q22685 caenorhabdi
28	198	20.9	1195	5	Q9N343	Q9N343 caenorhabdi
29	195	20.6	1391	5	O19021	O19021 caenorhabdi
30	194	20.5	1297	5	O9U350	O9U350 caenorhabdi
31	193	20.4	1474	5	O62504	O62504 caenorhabdi
32	192	20.3	491	4	O96S20	O96S20 homo sapien
33	192	20.3	548	4	Q96N28	Q96N28 homo sapien
34	188	19.8	751	13	Q9DGJ7	Q9DGJ7 gallus gall
35	186.5	19.7	747	13	Q91963	Q91963 xenopus. ap
36	186.5	19.7	984	5	O9GQ2	O9GQ2 calliactis
37	186.5	19.7	984	5	O9GQ1	O9GQ1 calliactis
38	186	19.6	484	4	O13793	O13793 homo sapien
39	186	19.6	547	4	O13764	O13764 homo sapien
40	186	19.6	770	6	Q9TUI0	Q9TUI0 sus scrofa
41	185.5	19.6	1203	5	O45916	O45916 caenorhabdi
42	183.5	19.4	607	11	O99K32	O99K32 mus musculus
43	183	19.3	160	11	O9QZ78	O9QZ78 cavia sp. p
44	178	18.8	1965	5	O61893	O61893 caenorhabdi
45	177	18.7	59	5	Q9TWF8	Q9TWF8 anemonia su

## ALIGNMENTS

### RESULT 1

Q969E0	PRELIMINARY;	PRT;	252 AA.
ID	Q969E0		
AC	Q969E0;		
DT	01-DEC-2001 (Tremblrel. 19, Created)		
DT	01-DEC-2001 (Tremblrel. 19, Last sequence update)		
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)		
DE	SERINE PROTEASE INHIBITOR, KUNITZ TYPE, 2.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=OVARY, AND ADENOCARCINOMA;		
RA	Strausberg R.;		
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=OVARY, AND ADENOCARCINOMA;		
RA	Strausberg R.;		
RL	Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=OVARY, AND ADENOCARCINOMA;		
RA	Strausberg R.;		
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC012868; AAH12868.1;		
DR	EMBL; BC007705; AAH07705.1;		
DR	EMBL; BC011951; AAH11951.1;		
DR	EMBL; BC011955; AAH11955.1;		
KW	Protease.		
SQ	SEQUENCE 252 AA; 28242 MW; FDD3360C1F3A7057 CRC64;		

Query Match 100.0%; Score 948; DB 4; Length 252;

Best Local Similarity 100.0%; Pred. No. 8.3e-93;

Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADERSIHDFCLVSKVGRG.....ACMLRCFRQENPPLGLSK 170

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|||||
Db 28 ADRSRTHDFCLVSKVGRCRASMPRWNVTDGSQLFYVGGCDGNSNNYLTKECLKK 87
QY 61 CATVTENATGDLATSNADSSVPSAPRQDSHSDMFNEEYCTANAVTGPCRASFP 120
Db 88 CATVTENATGDLATSNADSSVPSAPRQDSHSDMFNEEYCTANAVTGPCRASFP 147
QY 121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 170
Db 148 RWYFDVERNSCNNFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 197

RESULT 2
Q9D808 PRELIMINARY; PRT; 195 AA.
AC Q9D808:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE SERINE PROTEASE INHIBITOR, KUNITZ TYPE 2.
GN SPINT2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Willing L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK017792; BAB25258.1; -.
DR HSSP; P05067; 1AAP.
DR MGD; MGI:1338031; Spint2.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 195 AA; 21705 MW; 1ABD78CEFF1175DE1 CRC64;

Query Match 40.2%; Score 381; DB 11; Length 195;
Best Local Similarity 64.5%; Pred. No. 1.1e-32;
Matches 69; Conservative 14; Mismatches 24; Indels 0; Gaps 0;

QY 64 VTENATGDLATSNADSSVPSAPRQDSHSDMFNEEYCTANAVTGPCRASFP 123
Db 34 VHTNTDDMARNRNGADSVLSVPRQSDLSAEIFNEEYCVKAVTGPCRAEAPRWY 93
QY 124 FVERNSCNNFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 170
Db 94 YDEKNSCISFIYGGCRGNKNSYLSOEAQHCSGKQMPFLTPGLK 140
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RESULT 3
Q9D3K4 PRELIMINARY; PRT; 507 AA.
AC Q9D3K4:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE SERINE PROTEASE INHIBITOR, KUNITZ TYPE 1.
GN SPINT1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=HEAD;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Willing L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK017342; BAB30697.1; -.
DR HSSP; P05067; 1CA0.
DR MGD; MGI:1338033; Spint1.
DR InterPro; IPR002223; Kunitz_BPTI.
DR InterPro; IPR002172; LDL_recept_A.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00057; ldl_recept_a; 1.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 2.
DR SMART; SM00192; LDLa; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Serine protease inhibitor.
SQ SEQUENCE 507 AA; 56571 MW; 9EE0A29B7056D72D CRC64;

Query Match 31.0%; Score 294; DB 11; Length 507;
Best Local Similarity 32.4%; Pred. No. 5.8e-23;
Matches 59; Conservative 23; Mismatches 70; Indels 30; Gaps 3;

QY 5 RSHDFCLVSKVGRCRASMPRWNVTDGSQLFYVGGCDGNSNNYLTKECLKKCATV 64
Db 238 KOTEDYCLASYKVGRCGSPRMYVDPKQICKSFTEGCLGNKNKNLYREECMLACKDV 297
QY 65 -----TENATGDLATSNAD-----SSVPSAPRQDSHSDMFNEE- 104
Db 298 QGISPKRHHPCVSGCHATQFRCSNCCIDGFLCEDDTDCPDGSDTEATCEKXTSGDEL 357
QY 105 -----YCTANAVTGPCRASFPWYFDVERNSCNNFIYGGCRGNKNSYRSEACML 154
Db 358 QNIHFLSDKGYCAELPDTGTCKENIPRWYNPFSERCARFTYGGCYGNKNNEEQOOLE 417
QY 155 RC 156
Db 418 SC 419
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RC	STRAIN=BERKELEY;
RX	MEDLINE=20196006; PubMed=10731132;
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA	Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champagne M., Pfeiffer B.D.,
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.B.G.,
RA	Abriel J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA	Beeson K.V., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA	de Pablo J.B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA	Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA	Glocke A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA	Pallazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA	Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA	Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RT	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RL	"The genome sequence of Drosophila melanogaster.";
CC	Science 287:2185-2195(2000).
DR	-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A
DR	SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
DR	EMBL; AE003765; AAF56794.2; -
DR	EMBL; AE003765; AAF56795.2; -
DR	HSSP; p12111; 2KNT.
DR	FlyBase; FBgn0003137; Ppn.
DR	InterPro; IPR0003561; EGF-like.
DR	InterPro; IPR003598; Ig_C2.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR002223; Kunitz_BPTI.
DR	InterPro; IPR000884; TSPI.
DR	InterPro; IPR002221; WAP.
DR	Pfam; PF00047; ig_3.
DR	Pfam; PF00014; Kunitz_BPTI; 12.
DR	Pfam; PF00090; tsp_1; 5.
DR	Pfam; PF00095; wap; 1.
DR	PRINTS; PR00759; BASICPTASE.
DR	SMART; SM00408; IGC2; 3.
DR	SMART; SM00131; KU; 12.
DR	SMART; SM00209; TSPI; 7.
DR	SMART; SM00217; WAP; 1.
DR	PROSITE; PS00317; 4-DISULFIDE_CORE; 1.
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 11.
DR	PROSITE; PS00279; BPTI_KUNITZ_2; 12.
DR	PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR	PROSITE; PS00092; TSPI; 3.
DR	Alternative splicing; Immunoglobulin domain;
KW	Serine protease inhibitor.
FT	VARSPLIC 2803 2803
FT	VARSPLIC 2844 2854
FT	VARSPLIC 2855 3060
FT	VARSPLIC 3060 AA; 331579 MW; ACA31D3BE58C7C0 CRC64;
SEQ	SEQUENCE FROM N.A.

RESULT 4	
Q99J04	
ID	PRELIMINARY; PRT; 507 AA.
AC	
CD	
DT	01-JUN-2001 (TrEMBLrel. 17, Created)
DDT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE	SERINE PROTEASE INHIBITOR, KUNITZ TYPE 1.
GN	SPINT1.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_Taxid=10090;
OX	[1]
RP	SEQUENCE FROM N.A.
RA	Strausberg R.;
RRL	Submitted (Apr-2001) to the EMBL/GenBank/DDBJ databases.
EMBL	BC005769; AAH05769.1; -
EMBL	HSSP; P05067; lCAO.
MGD	MGI:1338033; Spintl.
DR	InterPro; IPR002223; Kunitz_BPTI.
DR	InterPro; IPR002172; LDL_recept_A.
DR	Pfam; PF00014; Kunitz_BPTI; 2.
DR	Pfam; PF00057; ldl_recept_a; 1.
DR	PRINTS; PR00759; BASICPTASE.
DR	SMART; SM00131; KU; 2.
DR	SMART; SM00192; LDLA; 1.
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR	PROSITE; PS00279; BPTI_KUNITZ_2; 2.
DR	PROSITE; PS01209; LDLRA_1; 1.
DR	PROSITE; PS00068; LDLRA_2; 1.
KW	Glycoprotein; Protease; Serine protease inhibitor.
SEQ	SEQUENCE 507 AA; 56590 MW; F7F9CCR2693D1F8D CRC64;

Query Match	31.0%; Score 294; DB 11; Length 507;
Best Local Similarity	32.4%; Pred. No. 5.8e-23;
Matches 59; Conservative 23; Mismatches 70; Indels 30; Gaps 3;	

QY	5	RSHTDFCLYSKVVGCRASPRWYNVTVGSCQLFYVGGCGNSNNYLTKEECLKKCATV	64
Db	238	KQTEDYCLASYKVGRCRGSPRWYDPKQICKSFYTGGLGNKNNYLRBEECLACKDV	297
QY	65	-----TENATGDLATSRNAAD-----SVPSAPRRQDSHDHSDMFNVEE-	104
Db	298	QGISPKRHHPCVSGSCHATFCRNGCCIDFLCEDDTPDCPDGSEATCEKYTSQDEL	357
QY	105	-----YCFANAVTGPCRASFPWWFDVNRNSCNFFIYGGCRGNKNSYRSEECML	154
Db	358	QNIFHLSDKGVCALPDGTGCKENIPRWYNPFSECARFYGGCYGNKNFNFEEOQCLE	417
QY	155	RC 156	
Db	418	SC 419	

RESULT 5	
Q9VAV4	

```
Query Match      27.3%; Score 259; DB 5; Length 3060;
Best Local Similarity 32.9%; Pred. No. 2.5e-18;
Matches 52; Conservative 16; Mismatches 66; Indels 24; Gaps 3;

QY 9 DFCLVSKVVGCRASMPRWYNTDGSQCLFYVGGCDGNSNNYLTKECLKCKCATVTENA 68
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1807 DICEIPAEGECANVYTSWYDTQACQRFYVGGCGGNNRFPTEESCLARCKRPEPT 1866
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 69 TGLATSRNAADSSVPSAPRQDSHSDMFNVEEYCTANAVTGPCRASFPFWYDFVER 128
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1867 TTTPTATR-----PQPSRQD-----VCDEEPAPGECSTWVLWKHFDRKI 1904
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 129 NSCNFIYGGCRGNKNSYSEAEACMLRCFRQENPPLP 166
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1905 GACRQFYVGGCGGNGRNFETENDCQRCLSQE--PPAP 1940
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
O44938
ID O44938 PRELIMINARY; PRT; 1572 AA.
AC O44938;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE THROMBOSPONDIN.
GN THRI.
OS Haemochus contortus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.
ON NCBI_TaxID=6289;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MOREDUN;
RA Skuce P.J., Newlands G.F.J., Stewart M., Pettit D., Smith D.,
RT "Cloning and characterization of thrombospondin, a novel multidomain
RT glycoprotein associated with the gut of Haemonchus contortus.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF043121; AAB99830.2; -.
DR HSSP: P05067; ICAO.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR002223; Kunitz_BPTI.
DR InterPro: IPR000884; TSPI.
DR Pfam: PF00014; Kunitz_BPTI; 12.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00001; EGF-like; 1.
DR SMART: SM00131; KU; 6.
DR SMART: SM00209; TSPI; 7.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 6.
DR PROSITE: PS50092; TSPI; 2.
KW Serine protease inhibitor.
FT SIGNAL 1 21
SQ SEQUENCE 1572 AA; 171871 MW; 2260B30DC2F903EC CRC64;

Query Match      27.1%; Score 256.5; DB 5; Length 1572;
Best Local Similarity 30.1%; Pred. No. 2.1e-18;
Matches 47; Conservative 21; Mismatches 61; Indels 27; Gaps 1;

QY 11 CLVSKVVGCRASMPRWYNTDGSQCLFYVGGCDGNSNNYLTKECLKCKCATVTENATG 70
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1394 CHLPDVGKCGGSDSWYEMATGSCVEFYKSCGNNRFASEBCECENTCV----- 1445
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 71 DLATSRNAADSSVPSAPRQDSHSDMFNVEEYCTANAVTGPCRASFPFWYDFVERNS 130
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1446 -----RHSEPHSDTTSHGTSVDEAKETGCTNFKTKWYKNADGT 1486
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 131 CNFIYGGCRGNKNSYSEAEACMLRCFRQENPPLP 166
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1487 CNRFHYGGCGEGTRNFDNQSCCKAACANHQDACLTP 1522
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
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Q9U8G8
ID Q9U8G8 PRELIMINARY; PRT; 3198 AA.
AC Q9U8G8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE LACUNIN PRECURSOR.
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Sphingioidea; Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99457716; PubMed=10528409;
RA Nardi J.B., Martos R., Walden K.K., Lampe D.J., Robertson H.M.;
RT "Expression of lacunin, a large multidomain extracellular matrix
RT protein, accompanies morphogenesis of epithelial monolayers in Manduca
RT sexta.";
RL Insect Biochem. Mol. Biol. 29:883-897(1999).
DR EMBL: AF078161; AAF04457.1; -.
DR HSSP: P12111; 2KNT.
DR InterPro: IPR004094; Antistatin.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR002223; Kunitz_BPTI.
DR InterPro: IPR000884; TSPI.
DR InterPro: IPR002221; WAP.
DR Pfam: PF02822; Antistatin; 4.
DR Pfam: PF00047; Ig; 2.
DR Pfam: PF00014; Kunitz_BPTI; 9.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00408; IGC2; 2.
DR SMART: SM00131; KU; 10.
DR SMART: SM00209; TSPI; 7.
DR SMART: SM00217; WAP; 1.
DR PROSITE: PS00317; 4-DISULFIDE_CORE; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 8.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 10.
DR PROSITE: PS50092; TSPI; 1.
KW Immunoglobulin domain; Serine protease inhibitor; Signal.
FT SIGNAL 1 21
SQ SEQUENCE 3198 AA; 349364 MW; AB4ACD459CD9134 CRC64;

Query Match      26.9%; Score 255; DB 5; Length 3198;
Best Local Similarity 31.7%; Pred. No. 6.9e-18;
Matches 51; Conservative 23; Mismatches 63; Indels 24; Gaps 3;

QY 9 DFCLVSKVVGCRASMPRWYNTDGSQCLFYVGGCDGNSNNYLTKECLKCKCATVTENA 68
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2133 DLCTLPAAIGDCADYRERWYDTPREKSCQRFYVGGCAGNGNFAQECBGR----- 2185
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 69 TGLATSRNAADSSVPSAPRQDSHSDMFNVEEYCTANAVTGPCRASFPFWYDFVER 128
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2186 -----SEAKITTVR--PTEAHP-----LTMCFMKEKDPGCTDTETRWVYDKL 2228
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 129 NSCNFIYGGCRGNKNSYSEAEACMLRCFRQENPPLP 169
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2229 GKCVTEYGGCGGNNRNFTEEYCYQYCGTAQDQCPLPMS 2269
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
O93424
ID O93424 PRELIMINARY; PRT; 287 AA.
AC O93424;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 33.1 KDA PROTEIN.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Ostariophysii;
```

OC Cypriniformes; Cyprinidae; Cyprinus.  
 OX NCBI\_TaxID=7962;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LIVER;  
 RA Gracey A.Y.;  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF008648; AAC19410.1; -  
 DR HSSP; P31713; LSHP.  
 DR InterPro; IPR002223; Kunitz\_BPTI.  
 DR Pfam; PF00014; Kunitz\_BPTI; 3.  
 DR PRINTS; PR00759; BASICPTASE.  
 DR SMART; SK00131; KU; 3.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 3.  
 DR PROSITE; PS0279; BPTI\_KUNITZ\_2; 3.  
 KW Hypothetical protein; Serine protease inhibitor.  
 SQ SEQUENCE 287 AA; 33093 MW; DF69B3D76718115E CRC64;  
  
 Query Match 26.6%; Score 252; DB 13; Length 287;  
 Best Local Similarity 30.9%; Pred. No. 8.8e-19;  
 Matches 50; Conservative 19; Mismatches 53; Indels 40; Gaps 3;  
  
 QY 8 HDCLVSKVVGRCRASPWWYVNTDGSQCLFYVGGCGNSNNYLKKECLKKCATVTEN 67  
 DB 39 HHSCKALKDEGCKALKDRFYFTDTGRGESFYGGCGQNNENFETLQCEKMLV---- 94  
  
 QY 68 ATGDLATSRNAADSSVPSAPRRDSEHSDMFENYEYCTANAVTGPCRASFPRWYFDVE 127  
 DB 95 -----KEDKSP-----CQLDDEPGPCRLVRYFFDFK 122  
  
 QY 128 RNSCNNFYGGCGRGNKNSRSEACMLRCF-----RQENPLP 165  
 DB 123 SQBCKRFFYGGCGFNGNFKTIKECHERCLPALNNMERNAPL 164  
  
 RESULT 9  
 O76840  
 ID O76840 PRELIMINARY; PRT; 2167 AA.  
 AC O76840; Q22911;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE C37C3.6 PROTEIN.  
 GN C37C3.6.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RA Geisel C., Bradshaw H.;  
 RT "The sequence of C. elegans cosmid C37C3";  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 CC -!- ALTERNATIVE PRODUCTS: TWO FORMS (A AND B) MAY BE PRODUCED BY  
 CC OF FORM B.  
 CC EMBL; U64857; AAC25868.1; -  
 CC EMBL; U64857; AAC25867.1; -  
 DR HSSP; P00981; LDTK.  
 DR InterPro; IPR003598; Ig\_c2.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR002223; Kunitz\_BPTI.  
 DR InterPro; IPR000884; TSPI.  
 DR Pfam; PF00047; Ig; 1.  
 DR Pfam; PF00014; Kunitz\_BPTI; 11.  
 DR Pfam; PF00090; tsp-1; 6.  
 DR PRINTS; PR00759; BASICPTASE.  
 DR SMART; SM00408; IGC2; 1.  
 DR SMART; SM00131; KU; 11.  
 DR SMART; SM00209; TSPI; 7.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 10.  
 DR PROSITE; PS0279; BPTI\_KUNITZ\_2; 11.

DR PROSITE; PS50092; TSPI; 4.  
 KW Alternative splicing; Hypothetical protein; Immunoglobulin domain;  
 KW Serine protease inhibitor.  
 FT VARSPLIC 147 155 MISSING (IN ISOFORM A).  
 FT VARSPLIC 1556 1558 KDD -> SKF (IN ISOFORM A).  
 FT VARSPLIC 1559 2167 MISSING (IN ISOFORM A).  
 SQ SEQUENCE 2167 AA; 237599 MW; 96274786D52E3639 CRC64;  
  
 Query Match 26.4%; Score 250.5; DB 5; Length 2167;  
 Best Local Similarity 30.1%; Pred. No. 1.3e-17;  
 Matches 49; Conservative 26; Mismatches 79; Indels 9; Gaps 1;  
  
 QY 5 RSIHDFCLVSKVVGRCRASPWWYVNTDGSQCLFYVGGCGNSNNYLKKECLKKC--- 61  
 DB 1265 QSMEDICRSRQDAGPCETYSQWYFNAFSECEFTFYGGCGNLNRRFSKDECEQRCFFV 1324  
  
 QY 62 -----ATVTENATGDLATSRNAADSSVPSAPRRDSEHSDMFENYEYCTANAVTGPC 115  
 DB 1325 HGAQPSAAQEQAPAAQAPQAPNSIVSPPOOSAPVVPVPSNKSORDACHLNVDOGRC 1384  
  
 QY 116 RASFPRWYFDVERNSCNNFYGGCGRGNKNSRSEACMLRCFR 158  
 DB 1385 KGAFDSWYEVATGSCVTKYTCGCGNANRFASKDOCESLCKV 1427  
  
 RESULT 10  
 Q9GQR0  
 ID Q9GQR0 PRELIMINARY; PRT; 2174 AA.  
 AC Q9GQR0;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE EXTRACELLULAR MATRIX PROTEIN PAPILIN PRECURSOR.  
 GN PPN  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DP CN BW;  
 RX MEDLINE=20530499; PubMed=11076767;  
 RA Kramerova I.A., Kawaguchi N., Nelson R.E., Fessler L.I., Chen Y.,  
 RA Kramerov A.A., Kusche-Gullberg M., Kramer J.M., Ackley B.D.,  
 RA Sieron A.L., Prockop D.J., Fessler J.H.;  
 RT "Papilin in development; a pericellular protein with a homology to the  
 RT ADAMTS metalloproteinases";  
 RL Development 127:5475-5485(2000).  
 DR EMBL; AF205357; AAG37995.1; -  
 DR HSSP; P12111; 2KNT.  
 DR FlyBase; FBgn0003137; Ppn.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR003598; Ig\_c2.  
 DR InterPro; IPR003600; Ig\_Like.  
 DR InterPro; IPR002223; Kunitz\_BPTI.  
 DR InterPro; IPR000884; TSPI.  
 DR InterPro; IPR002221; WAP.  
 DR Pfam; PF00014; Kunitz\_BPTI; 3.  
 DR PRINTS; PR00003; 4DISULPHCORE.  
 DR PRINTS; PR00759; BASICPTASE.  
 DR SMART; SM00409; IG; 3.  
 DR SMART; SM00408; IGC2; 2.  
 DR SMART; SM00410; IG\_Like; 1.  
 DR SMART; SM00131; KU; 3.  
 DR SMART; SM00209; TSPI; 7.  
 DR SMART; SM00217; WAP; 1.  
 DR PROSITE; PS50279; BPTI\_KUNITZ\_2; 3.  
 DR PROSITE; PS50092; TSPI; 3.  
 KW Matrix protein; Serine protease inhibitor; Signal.  
 FT SIGNAL 1 26 POTENTIAL.  
 SQ SEQUENCE 2174 AA; 231936 MW; 038F707952623120 CRC64;



DR PRINTS; PR00759; BASICPTASE.

DR SMART; SM00131; KU; 3.

DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 3.

DR PROSITE; PS00279; BPTI\_KUNITZ\_2; 3.

KW Serine protease inhibitor.

SQ SEQUENCE 396 AA; 43948 MW; 50F65C8337A003D9 CRC64;

Query Match 25.3%; Score 239.5; DB 6; Length 396;  
Best Local Similarity 29.6%; Pred. No. 2.7e-17;  
Matches 45; Conservative 24; Mismatches 60; Indels 23; Gaps 1;

QY 5 RSTHCLVSKVVGRCRASPRWYNTDGSOLFVYGGDGNNSNYLTKEECLKKCATV 64

DB 47 RLHSFCALKADNGPCRAMRNTFFNIHTQCEEFYGGCGNQNRFSLECEECVVR 106

QY 65 TENATGLATSRNAADSSVPSAPRRQDSHSDMFNIEYCTANAVTGPCRASFPRWY 124

DB 107 YPKA-----KTELEKVLKPDYCHMNEDESLCRGFVTRY 143

QY 125 DVERNSCNNFIYGGCRGNKNSYSEACMLRC 156

DB 144 NVSSKCEGFYGGCLGNLNNFETLEQCKNTC 175

RESULT 14

Q9DBJ9

ID Q9DBJ9 PRELIMINARY; PRT; 349 AA.

AC Q9DBJ9;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE ALPHA 1 MICROGLOBULIN/BIKUNIN.

GN AMBP.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RT [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=LIVER;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schirali L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Cariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashizaki Y.

RT "Functional annotation of a full-length mouse cDNA collection."

RL Nature 409:685-690(2001).

DR EMBL; AK004907; BAB23659.1;

DR HSSP; P02760; 1BIK.

DR MGD; MGI:88002; Ambp.

DR InterPro; IPR002223; Kunitz\_BPTI.

DR InterPro; IPR002345; Lipocalin.

DR Pfam; PF00014; Kunitz\_BPTI; 2.

DR Pfam; PF00061; lipocalin; 1.

DR PRINTS; PR00759; BASICPTASE.

DR PRINTS; PR00179; LIPOCALIN.

DR SMART; SM00131; KU; 2.

DR PROSITE; PS00279; BPTI\_KUNITZ\_2; 2.

DR PROSITE; PS00213; LIPOCALIN; UNKNOWN\_1.

KW Serine protease inhibitor.

SQ SEQUENCE 349 AA; 39101 MW; E593222FBC01BC3D CRC64;

Query Match 24.8%; Score 235.5; DB 11; Length 349;

Best Local Similarity 29.7%; Pred. No. 6.2e-17;

Matches 44; Conservative 18; Mismatches 47; Indels 39; Gaps 1;

QY 9 DFCLVSKVVGRCRASPRWYNTDGSOLFVYGGDGNNSNYLTKEECLKKCATV 68

DB 228 DSCQLNYSSEGPCLGMOERYIYNGASMACETFFYGGCLGNGNFISEKDCLOTCTTAA-- 285

QY 69 TGDLATSRNAADSSVPSAPRRQDSHSDMFNIEYCTANAVTGPCRASFPWYFDV 128

DB 286 -----CNLPVQGPCRAFIKLWAFDAQA 308

QY 129 NSCNNFIYGGCRGNKNSYSEACMLRC 156

DB 309 GKCIQHYGGCGKNGNKFYSEKCEKCYC 336

RESULT 15

Q925W1

ID Q925W1 PRELIMINARY; PRT; 349 AA.

AC Q925W1;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE ALPHA-1-MICROGLOBULIN/BIKUNIN PRECURSOR.

GN AMBP.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RT [1]

RP SEQUENCE FROM N.A.

RC STRAIN=129SV;

RX MEDLINE=99326507; PubMed=10395906;

RA Lindqvist A., Rouet P., Salier J.P., Akerstrom B.,

RT "The alpha1-microglobulin/bikunin gene: characterization in mouse and

evolution."

RL Gene 234:329-336(1999).

DR EMBL; AF034692; AAD01995.1; -

FT SIGNAL 1 19 POTENTIAL.

FT CHAIN 20 349 ALPHA-1-MICROGLOBULIN/BIKUNIN.

SQ SEQUENCE 349 AA; 39029 MW; CFB9208D37DF0021 CRC64;

Query Match 24.8%; Score 235.5; DB 11; Length 349;

Best Local Similarity 29.7%; Pred. No. 6.2e-17;

Matches 44; Conservative 18; Mismatches 47; Indels 39; Gaps 1;

QY 9 DFCLVSKVVGRCRASPRWYNTDGSOLFVYGGDGNNSNYLTKEECLKKCATV 68

DB 228 DSCQLNYSSEGPCLGMOERYIYNGASMACETFFYGGCLGNGNFISEKDCLOTCTTAA-- 285

QY 69 TGDLATSRNAADSSVPSAPRRQDSHSDMFNIEYCTANAVTGPCRASFPWYFDV 128

DB 286 -----CNLPVQGPCRAFIKLWAFDAQA 308

QY 129 NSCNNFIYGGCRGNKNSYSEACMLRC 156

DB 309 GKCIQHYGGCGKNGNKFYSEKCEKCYC 336

Search completed: October 18, 2002, 10:35:49

Job time : 33 secs





GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 18, 2002, 10:33:48 ; Search time 12 Seconds  
(without alignments)  
548.527 Million cell updates/sec

Title: us-09-218-913d-52

Perfect score: 948

Sequence: 1 ADERSIHDFCLVSKVGRG.....ACMLRCFRQENPLPLGSK 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	948	100.0	252	1 SPT2_HUMAN	O43291 homo sapien
2	663	69.9	252	1 SPT2_MOUSE	Q9W403 mus musculus
3	312	32.9	513	1 SPT1_HUMAN	O43278 homo sapien
4	294	31.0	507	1 SPT1_MOUSE	Q9R097 mus musculus
5	259.5	27.4	306	1 TFPI_MOUSE	O54819 mus musculus
6	249.5	26.3	352	1 AMBP_BOVIN	P00978 bos taurus
7	247.5	26.1	346	1 AMBP_MERUN	O62577 meriones un
8	246.5	26.0	302	1 TFPI_RAT	Q02445 rattus norv
9	244.5	25.8	123	1 IATR_SHEEP	P13371 ovis-aries
10	244.5	25.8	352	1 AMBP_HUMAN	P02760 homo sapien
11	244	25.7	300	1 TFPI_RABIT	P19761 oryctolagus
12	242.5	25.6	337	1 AMBP_PTG	P04366 sus scrofa
13	241.5	25.5	123	1 IATR_HORSE	P04365 equus caball
14	237.5	25.1	349	1 AMBP_RAT	Q64240 rattus norv
15	236.5	24.9	304	1 TFPI_MACMU	Q28864 macaca mula
16	235.5	24.8	349	1 AMBP_MESAU	Q60559 mesocricetu
17	235.5	24.8	304	1 AMBP_MOUSE	Q07456 homo sapien
18	233.5	24.6	304	1 TFPI_HUMAN	P10646 homo sapien
19	214.5	22.6	235	1 TFPI_HUMAN	P48307 homo sapien
20	210	22.2	765	1 APP2_RAT	P15943 rattus norv
21	204.5	21.6	230	1 TFPI_MOUSE	O35536 mus musculus
22	200	21.1	763	1 APP2_HUMAN	Q06481 homo sapien
23	191	20.1	1416	1 YN81_CAEEL	Q03610 caenorhabdi
24	187.5	19.8	770	1 A4_RAT	P08592 rattus norv
25	186	19.6	751	1 A4_SAISC	Q95241 salminki scl
26	186	19.6	770	1 A4_MOUSE	P05067 homo sapien
27	183.5	19.4	770	1 AMBP_PLEPL	P12023 mus musculus
28	181.5	19.1	355	1 AMBP_PLEPL	P36992 pleuronecte
29	175.5	18.5	69	1 CRPT_BOOMI	P81162 boophilus m
30	174.5	18.4	76	1 A4_MACMU	P29216 macaca mula
31	174.5	18.4	87	1 A4_MACFA	P53601 macaca fasc
32	171.5	18.1	197	1 MCP1_MELCP	P82968 melithaea c
33	170	17.9	58	1 AXP1_ANTAF	P81547 anthoplaura

## RESULT 1

ID	SPT2_HUMAN	STANDARD;	PRT;	252 AA.
AC	O43291; O00271; O14895; Q969E0;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Kunitz-type protease inhibitor 2 precursor (Hepatocyte growth factor activator inhibitor type 2) (HAI-2) (Placental bikunin).			
DE	SPINT2 OR HAI2 OR KOP.			
GN	Homo sapiens (Human).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98010584; PubMed=9346890;			
RA	Kawaguchi T., Qin L., Shimomura T., Kondo J., Matsumoto K., Denda K.,			
RA	Kitamura N.;			
RT	"Purification and cloning of hepatocyte growth factor activator			
RT	inhibitor type 2, a Kunitz-type serine protease inhibitor.";			
RL	J. Biol. Chem. 272:27558-27564(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 28-74.			
RC	TISSUE=Placenta;			
RX	MEDLINE=97277372; PubMed=9115294;			
RA	Marlor C.W., Delaria K.A., Davis G., Muller D.K., Greve J.M.,			
RA	Tamburini P.P.;			
RT	"Identification and cloning of human placental bikunin, a novel serine			
RT	protease inhibitor containing two Kunitz domains.";			
RL	J. Biol. Chem. 272:12202-12208(1997).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Pancreatic cancer;			
RX	MEDLINE=98094245; PubMed=9434156;			
RA	Mueller-Pillasch F., Wallrapp C., Bartels K., Varga G., Friess H.,			
RA	Buechler M., Adler G., Gress T.M.;			
RT	"Cloning of a new Kunitz-type protease inhibitor with a putative			
RT	transmembrane domain overexpressed in pancreatic cancer.";			
RL	Biochim. Biophys. Acta 1395:88-95(1998).			
RN	[4]			
RP	SEQUENCE FROM N.A., AND VARIANT LEU-200.			
RC	TISSUE=Colon, and Ovary;			
RX	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: INHIBITOR OF HGF ACTIVATOR. ALSO INHIBITS PLASMIN,			
CC	PLASMA AND TISSUE KALLIKREIN, AND FACTOR XIA.			
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).			
CC	-!- TISSUE SPECIFICITY: EXPRESSED IN PLACENTA, KIDNEY, PANCREAS,			
CC	PROSTATE, TESTIS, THYMUS, AND TRACHEA.			
CC	-!- DOMAIN: THIS INHIBITOR CONTAINS TWO INHIBITORY DOMAINS.			
CC	-!- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.			
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			

## ALIGNMENTS

34	167	17.6	62	1	IP52_ANESU
35	159	16.8	133	1	EPPI_HUMAN
36	159	16.8	265	1	TKD1_SHEEP
37	156	16.5	64	1	SPT3_HUMAN
38	156	16.5	164	1	TKD1_BOVIN
39	155.5	16.4	133	1	EPPI_MACMU
40	155	16.4	60	1	IBPS_BOVIN
41	155	16.4	100	1	BPT2_BOVIN
42	153	16.1	61	1	IBPI_TACTR
43	152.5	16.1	100	1	BPT1_BOVIN
44	152	16.0	65	1	IVB3_VIPAA
45	152	16.0	134	1	EPPI_MOUSE

P10280	anemonia su
O95925	homo sapien
Q29428	ovis aries
P49233	homo sapien
Q28201	bos taurus
Q9bd11	macaca mula
P00975	bos taurus
P04815	bos taurus
P16044	tachyplesus
P00974	bos taurus
P00992	vipera ammo
Q9da01	mus musculus

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EMBL: AB006534; BAA25024.1; -  
EMBL: U78095; AAC02781.1; -  
EMBL: AF027205; AAB84031.1; -  
EMBL: BC001668; AAH01668.1; -  
EMBL: BC007705; AAH07705.1; -  
EMBL: BC011951; AAH11951.1; -  
EMBL: BC011955; AAH11955.1; -  
EMBL: BC012868; AAH12868.1; -  
HSSP: P05067; ITAW.  
MIM: 605124; -

InterPro: IPR002223; Kunitz\_BPTI.  
Pfam: PF00014; Kunitz\_BPTI; 2.  
PRINTS: PR00759; BASICPTASE.  
SMART: SM00131; KU; 2.  
PROSITE: PS00280; BPTI\_KUNITZ\_1; 2.  
PROSITE: PS0279; BPTI\_KUNITZ\_2; 2.

Serine protease inhibitor; Repeat; Glycoprotein; Transmembrane; Signal; Polymorphism.  
FT SIGNAL 1 27

FT CHAIN 28 252 KUNITZ-TYPE PROTEASE INHIBITOR 2.  
FT DOMAIN 28 197 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 198 218 POTENTIAL.  
FT DOMAIN 219 252 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 38 88 BPTI/KUNITZ INHIBITOR 1.  
FT DOMAIN 133 183 BPTI/KUNITZ INHIBITOR 2.  
FT DISULFID 38 88 BY SIMILARITY.  
FT DISULFID 47 71 BY SIMILARITY.  
FT DISULFID 63 84 BY SIMILARITY.  
FT ACT\_SITE 48 49 REACTIVE BOND (BY SIMILARITY).  
FT DISULFID 133 183 BY SIMILARITY.  
FT DISULFID 142 166 BY SIMILARITY.  
FT DISULFID 158 179 BY SIMILARITY.  
FT ACT\_SITE 143 144 REACTIVE BOND (BY SIMILARITY).  
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 94 94 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARIANT 200 200 V -> L.  
FT CONFLICT 3 3 /FTIQ-VAR\_012482.  
FT CONFLICT 11 11 R -> H (IN REF. 3).  
FT CONFLICT 53 53 R -> P (IN REF. 1).  
FT CONFLICT 240 240 R -> K (IN REF. 3).  
FT CONFLICT 240 240 D -> H (IN REF. 3).  
SQ SEQUENCE 252 AA; 28228 MW; A7D3360C0EECA2B CRC64;

Query Match 100.0%; Score 948; DB 1; Length 252;  
Best Local Similarity 100.0%; Pred. No. 3.1e-83;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADERSIHDFCLVSKVVGRCRAMPWWNVTDGSQLFVYGGCDGNSNNYLTKESCLKK 60  
DB 28 ADERSIHDFCLVSKVVGRCRAMPWWNVTDGSQLFVYGGCDGNSNNYLTKESCLKK 87  
QY 61 CATVTENATGDLATSNAAADSSVPSAPRQDSHSDMFENYEYCTANAVGPCRASPP 120  
DB 88 CATVTENATGDLATSNAAADSSVPSAPRQDSHSDMFENYEYCTANAVGPCRASPP 147  
QY 121 RWYFDVERNSNNFIYGGCRGNKNSYRSEACMLRCFRQENPPLGSK 170  
DB 148 RWYFDVERNSNNFIYGGCRGNKNSYRSEACMLRCFRQENPPLGSK 197  
RESULT 2  
ID SPT2\_MOUSE STANDARD; PRT; 252 AA.  
AC Q9WU03; Q9WU04; Q9WU05;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Kunitz-type protease inhibitor 2 precursor (Hepatocyte growth factor

DE activator inhibitor type 2) (HAI-2).  
GN SPINT2 OR HAI2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RC STRAIN=BALB/C;  
RX MEDLINE=99160423; PubMed=10049781;  
RA Itoh H., Kataoka H., Hamasuna R., Kitamura N., Koono M.;  
RT "Hepatocyte growth factor activator inhibitor type 2 lacking the first  
Kunitz-type serine proteinase inhibitor domain is a predominant  
product in mouse but not in human";  
RL Biochem Biophys Res Commun. 255:740-748(1999).  
CC -!- FUNCTION: INHIBITOR OF HGF ACTIVATOR.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE  
CC PRODUCED BY ALTERNATIVE SPLICING.  
CC -!- TISSUE SPECIFICITY: ISOFORM 2 IS MORE PREDOMINANTLY EXPRESSED THAN  
CC ISOFORM 1.  
CC -!- DOMAIN: THIS INHIBITOR CONTAINS TWO INHIBITORY DOMAINS.  
CC -!- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.  
CC  
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EMBL: AF099016; AAD22172.1; -  
EMBL: AF099019; AAD22173.1; -  
EMBL: AF099020; AAD22174.1; -  
HSSP: P05067; ITAW.  
DR MGD; MGI:1338031; Spint2.  
DR InterPro: IPR002223; Kunitz\_BPTI.  
DR Pfam: PF00014; Kunitz\_BPTI; 2.  
DR PRINTS: PR00759; BASICPTASE.  
DR SMART; SM00131; KU; 2.  
DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 2.  
DR PROSITE; PS0279; BPTI\_KUNITZ\_2; 2.  
KW Serine protease inhibitor; Repeat; Glycoprotein; Transmembrane;  
Signal; Alternative splicing. POTENTIAL.  
FT SIGNAL 1 27  
FT CHAIN 28 252 KUNITZ-TYPE PROTEASE INHIBITOR 2.  
FT DOMAIN 28 197 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 198 218 POTENTIAL.  
FT DOMAIN 219 252 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 38 88 BPTI/KUNITZ INHIBITOR 1.  
FT DOMAIN 133 183 BPTI/KUNITZ INHIBITOR 2.  
FT DISULFID 38 88 BY SIMILARITY.  
FT DISULFID 47 71 BY SIMILARITY.  
FT DISULFID 63 84 BY SIMILARITY.  
FT ACT\_SITE 48 49 REACTIVE BOND (BY SIMILARITY).  
FT DISULFID 133 183 BY SIMILARITY.  
FT DISULFID 142 166 BY SIMILARITY.  
FT DISULFID 158 179 BY SIMILARITY.  
FT ACT\_SITE 143 144 REACTIVE BOND (BY SIMILARITY).  
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 94 94 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARSPLIC 114 128 PKQSAEDLSAEIFN -> CFVELSVAALFLFYA (IN  
FT ISOFORM 3).  
FT VARSPLIC 129 252 MISSING (IN ISOFORM 3).  
SQ SEQUENCE 252 AA; 27914 MW; B2FF4B86924D4F8F CRC64;  
Query Match 69.9%; Score 663; DB 1; Length 252;  
Best Local Similarity 68.2%; Pred. No. 4.1e-56;  
Matches 116; Conservative 21; Mismatches 33; Indels 0; Gaps 0;

QY 1 ADERSIHDFCLVSKVVGRCRAMPWWNVTDGSQLFVYGGCDGNSNNYLTKESCLKK 60

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Db 28 ASRELDVHSCGSKVYVGRASIPRWNYITDSCQPEVYGCENYQSKKECLDK 87
QY 61 CATVTENATGDLTNAADSPVSPAPRODSEHSSDMFENYECTANAVTGPCRASEP 120
Db 88 CAGVTENTDDWARRNGADSSVLSVPRQSAEDLSAEIFNYYEYCVPRAVTGPCRAAP 147
QY 121 RMYFDVNRSCNNFYGGCGKNGKNSYSEACMLRCFROQENPPLPLGSK 170
Db 148 RMYDTEKNSCISFYGGCGKNGKNSYLSQACMQHSCGQKMHPLTPGLK 197

RESULT 3
SPTL_HUMAN
ID SPTL_HUMAN STANDARD; PRT; 513 AA.
AC O43278;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Kunitz-type protease inhibitor 1 precursor (Hepatocyte growth factor
DE activator inhibitor type 1) (HAI-1).
GN SPINT1 OR HAI1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97197808; PubMed=9045658;
RA Shimomura T., Denda K., Kitamura A., Kawaguchi T., Kito M., Kondo J.,
RA Kagaya S., Qin L., Takata H., Miyazawa K., Kitamura N.;
RT "Hepatocyte growth factor activator inhibitor, a novel Kunitz-type
RT serine protease inhibitor."
RL J. Biol. Chem. 272:6370-6376(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (Mar-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP PARTIAL SEQUENCE, AND CHARACTERIZATION.
RC TISSUE=Milk;
RX MEDLINE=99303582; PubMed=10373425;
RA Lin C.Y., Anders J., Johnson M., Dickson R.B.;
RT "Purification and characterization of a complex containing matrilysin
RT and a Kunitz-type serine protease inhibitor from human milk."
RL J. Biol. Chem. 274:19237-19242(1999).
CC -!- FUNCTION: INHIBITOR OF HGF ACTIVATOR. ALSO ACTS AS AN INHIBITOR OF
CC MATRIPTASE (ST14).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DOMAIN: THIS INHIBITOR CONTAINS TWO INHIBITORY DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.
CC -!- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.
CC
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CC
CC EMBL; AB000095; BAA25014.1;
CC EMBL; BC004140; AA04140.1;
CC HSSP; P31713; 1SHP.
CC MIM; 605123;
CC InterPro; IPR002223; Kunitz_BPTI.
CC InterPro; IPR002172; LDL_recept_A.
CC Pfam; PF00014; Kunitz_BPTI; 2
CC Pfam; PF00057; ldl_recept_a; 1.
CC PRINTS; PR00759; BASICPTASE.
CC SMART; SM00131; KU; 2.
CC SMART; SM00192; LDLa; 1.
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DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS01209; LDLA_1; 1.
DR PROSITE; PS00068; LDLA_2; 1.
KW Serine protease inhibitor; Repeat; Glycoprotein; Signal.
FT SIGNAL 1 35
FT CHAIN 36 513 KUNITZ-TYPE PROTEASE INHIBITOR 1.
FT DOMAIN 250 300 BPTI/KUNITZ INHIBITOR 1.
FT DOMAIN 318 354 LDL-RECEPTOR CLASS A.
FT DOMAIN 375 425 BPTI/KUNITZ INHIBITOR 2.
FT DISULFID 250 300 BY SIMILARITY.
FT DISULFID 259 283 BY SIMILARITY.
FT DISULFID 275 296 BY SIMILARITY.
FT ACT_SITE 260 261 REACTIVE BOND (BY SIMILARITY).
FT DISULFID 375 425 BY SIMILARITY.
FT DISULFID 384 408 BY SIMILARITY.
FT ACT_SITE 385 386 REACTIVE BOND (BY SIMILARITY).
FT CARBOHYD 56 66 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 235 235 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 507 507 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 513 AA; 56885 MW; D6E05F3A5885CDDD CRC64;

Query Match 32.9%; Score 312; DB 1; Length 513;
Best Local Similarity 33.5%; Pred. No. 2.3e-22;
Matches 67; Conservative 24; Mismatches 71; Indels 38; Gaps 5.

QY 5 RSHDFCLVSKVVGRCRSMRWNVDTGSCOLFVYGGDGNNSNLYLKEECLKKCATV 64
Db 244 KOTEDYCLASNKVYGRGSRFPWYDPTQICKYVGGCLGNKLYREECILACRGV 303
QY 65 -----TENATGDLATSRNAADS-----SVPSAPRRQDS---EDHSSDMFNY 102
Db 304 QGPMERRHPVCSGTQPTQFCRSCNGCCIDSFLECDTTPNCPDASDEACEKYTSFDEL 363
QY 103 EE-----YCTANAVTGPCRASFPRWYFDVVERNSCNNFIYGGCGKNGKNSYSEACML 154
Db 364 QRHFPSDKGHCVLDPTDGLCKESIPRWYNPSEHCARFTYGGCYGNKNFEEQOCLE 423
QY 155 RC-----FRQENPPLP 166
Db 424 SCRGISKDVFGRLRREIP 443

RESULT 4
SPTL_MOUSE
ID SPTL_MOUSE STANDARD; PRT; 507 AA.
AC Q9R097;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kunitz-type protease inhibitor 1 precursor (Hepatocyte growth factor
DE activator inhibitor type 1) (HAI-1).
GN SPINT1 OR HAI1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C;
RA Itoh H., Kataoka H., Koono H.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INHIBITOR OF HGF ACTIVATOR (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- DOMAIN: THIS INHIBITOR CONTAINS TWO INHIBITORY DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.
CC -!- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.
CC
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CC EMBL; AF099018; AAF02490.1; -.
DR HSSP; P05067; ITAW.
DR MGD; MGI:1338033; Spint1.
DR InterPro; IPR002223; Kunitz_BPTI.
DR InterPro; IPR002172; LDL_recept_A.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00057; LDL_recept_a; 1.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 2.
DR SMART; SM00192; LDLa; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS01209; LDLRA_1; FALSE_NEG.
DR PROSITE; PS00068; LDLRA_2; 1.
KW Serine protease inhibitor; Repeat; Glycoprotein; Signal.
FT SIGNAL 1 29
FT CHAIN 30 507
FT DOMAIN 244 294
FT DOMAIN 312 348
FT DOMAIN 369 419
FT DISULFID 244 294
FT DISULFID 253 277
FT DISULFID 269 290
FT ACT_SITE 254 255
FT DISULFID 369 419
FT DISULFID 378 402
FT DISULFID 394 415
FT ACT_SITE 379 380
FT CARBOHYD 229 229
FT CARBOHYD 501 501
SQ SEQUENCE 507 AA; 56676 MW; 20CB5DEDCFE46AA7 CRC64;

Query Match
Best Local Similarity 31.0%; Score 294; DB 1; Length 507;
Matches 59; Conservative 23; Mismatches 66; Indels 30; Gaps 3;

QY 9 DFLVSKVVGRCRASHPRWYVNTDGSOLFVYGGCDGNSNNYKBECLKKCATV---- 64
Db 242 DYCLASYKVGRCRSHPRWYVNTDGSOLFVYGGCDGNSNNYKBECLKKCATV---- 64
QY 65 -----TENATGLATSNAD-----SSVPSAPRQDSHSDMFNYEE----- 104
Db 302 PKRHHPVCGSGCHATQFRCNSGCSIDGLECDTDPDGDSDCATCEKYTSFGDELQNIH 361
QY 105 -----YCTANAVTGPCRASHPRWYVNTDGSOLFVYGGCDGNSNNYKBECLKKCATV 156
Db 362 FLSDKGYCAELPDTGFCRKNIPRWYVNTDGSOLFVYGGCDGNSNNYKBECLKKCATV 419

RESULT 5
ID TFPI_MOUSE STANDARD; PRT; 306 AA.
AC 054819; 092208;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Tissue factor pathway inhibitor precursor (TFPI) (Lipoprotein-
DE associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)
DE (EPI).
GN TFPI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC STRAIN=129;
RX MEDLINE=98152575; PubMed=9493581;

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RA "Cloning, expression, and characterization of mouse tissue factor
RT pathway inhibitor (TFPI)".
RL Thromb. Haemost. 79:306-309(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RX MEDLINE=99138770; PubMed=9974373;
RA Chang J.-Y., Monroe D.M., Oliver J.A., Roberts H.R.;
RT "TFPIbeta, a second product from the mouse tissue factor pathway
RT inhibitor (TFPI) gene.";
RL Thromb. Haemost. 81:45-49(1999).
CC -!- FUNCTION: INHIBITS FACTOR X (X(A)) DIRECTLY AND, IN A XA-DEPENDENT
CC WAY, INHIBITS VII(A)/TISSUE FACTOR ACTIVITY, PRESUMABLY BY FORMING
CC A QUATERNARY X(A)/LACI/VII(A)/TF COMPLEX. IT POSSESSES AN
CC ANTITHROMBOTIC ACTION AND ALSO THE ABILITY TO ASSOCIATE WITH
CC LIPOPROTEINS IN PLASMA (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; alpha/TFPIalpha (shown here) and
CC beta/TFPIbeta; are produced by alternative splicing.
CC -!- TISSUE SPECIFICITY: Isoform alpha is expressed in heart and
CC spleen; isoform beta in heart and lung.
CC -!- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
CC -!- SIMILARITY: CONTAINS 3 BPTI/KUNITZ INHIBITOR DOMAINS.
CC -----
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DR EMBL; AF004833; AAC40035.1; -.
DR EMBL; AF016313; AAD01586.1; -.
DR HSSP; PI0646; ITPX.
DR MGD; MGI:1095418; Tfpi.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 3.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 3.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 3.
KW Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation;
KW Signal; Alternative splicing.
FT SIGNAL 1 28
FT CHAIN 29 306
FT DOMAIN 50 100
FT DOMAIN 121 171
FT DOMAIN 225 275
FT DISULFID 50 100
FT DISULFID 59 83
FT DISULFID 75 96
FT ACT_SITE 60 61
FT DISULFID 121 171
FT DISULFID 130 154
FT DISULFID 146 167
FT ACT_SITE 131 132
FT DISULFID 225 275
FT DISULFID 234 258
FT DISULFID 250 271
FT ACT_SITE 235 236
FT CARBOHYD 141 141
FT CARBOHYD 254 254
FT CARBOHYD 264 264
FT CARBOHYD 282 282
FT VARSPPLIC 218 253
FT VARSPPLIC 254 306
FT CONFLICT 68 68
FT CONFLICT 306 AA; 34987 MW; D3EA3297E4B6A359 CRC64;
SQ SEQUENCE


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Query Match 27.4%; Score 259.5; DB 1; Length 306;  
Best Local Similarity 33.3%; Pred. No. 1.3e-17;  
Matches 55; Conservative 21; Mismatches 64; Indels 25; Gaps 3;  
QY 9 DFCVSKVYVGRASPRWYNTVDSQQLFYVGGDGNSSNYLTKEECLKKCAT----- 63  
DB 119 DFCFLEEDPGLCRGMYKRLYNNQTCERFVYGGCLGRNNFETLDECKKICENPVHSP 178  
QY 64 -----VTE-NATGDLATSRNAADSSVPSAPRRODSEHDSSDMENYEYCTANAV 111  
DB 179 SPVNEVQMSDYVDGNTVDSTVNIVVPSQPKVPRRD-----YGRPWCLQPAD 230  
QY 112 TGPCRASFPWYEDVERNSCNNFYGGCGKNSYSEACMLRC 156  
DB 231 SGLCKASERREFFYNSATGKCHRENYTCGCGNNNFTTRRLRSC 275  
RESULT 6  
ID AMBP\_BOVIN STANDARD; PRT; 352 AA.  
AC P00978; P35420; Q28020;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE AMBP protein precursor [Contains: Alpha-1-microglobulin; Inter-alpha-  
trypsin inhibitor light chain (ITI-LC) (Bikunin) (HI-30) (BI-14)  
(Cumulus extracellular matrix stabilizing factor) (ESF)].  
DE AMBP OR ITIL.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP TISSUE=Liver;  
RC MEDLINE=96201710; PubMed=8611630;  
RX Lindqvist A., Akerstrom B.;  
RA "Bovine alpha 1-microglobulin/bikunin. Isolation and characterization  
of liver cDNA and urinary alpha 1-microglobulin.";  
RL Biochim. Biophys. Acta 1306:98-106(1996).  
RN [2]  
RP SEQUENCE OF 227-349.  
RX MEDLINE=85225967; PubMed=2408637;  
RA Hochstrasser K., Wachter E., Albrecht G.J., Reisinger P.;  
RT "Kunitz-type proteinase inhibitors derived by limited proteolysis of  
the inter-alpha-trypsin inhibitor, VII. Determination of the  
amino-acid sequence of the trypsin-released inhibitor from bovine  
inter-alpha-trypsin inhibitor.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 364:1679-1687(1983).  
RN [4]  
RP SEQUENCE OF 206-219.  
RC TISSUE=Fetal serum;  
RX MEDLINE=92291130; PubMed=1376324;  
RA Chen L., Mao S.J.T., Larsen W.J.;  
RT "Identification of a factor in fetal bovine serum that stabilizes the  
cumulus extracellular matrix. A role for a member of the inter-alpha-  
trypsin inhibitor family.";  
RL J. Biol. Chem. 267:12380-12386(1992).  
RN [5]  
RP REACTIVE SITES  
RX MEDLINE=84133808; PubMed=6199276;  
RA Hochstrasser K., Albrecht G.J., Schoenberger O.L., Wachter E.;  
RT "Kunitz-type proteinase inhibitors derived by limited proteolysis of  
the inter-alpha-trypsin inhibitor, VII. Characterization of the  
Hoppe-Seyler's Z. Physiol. Chem. 364:1689-1696(1983).  
RT FUNCTION: ALPHA-1-MICROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL  
FLUIDS INCLUDING PLASMA, URINE, AND CEREBROSPINAL FLUID. IT  
APPEARS NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH IGA  
AND ALBUMIN.  
RT FUNCTION: INTER-ALPHA-TRYPsin INHIBITOR, PRESENT IN PLASMA AND  
URINE, INHIBITS TRYPSIN, PLASMIN, AND LYSOSOMAL GRANULOCYTIC  
ELASTASE.  
RT FUNCTION: MAY DIFFUSE INTO FOLLICULAR FLUID AFTER AN OVULATORY  
STIMULUS TO ACT AS STRUCTURAL LINKER THAT ENSURE NORMAL CUMULUS  
EXPANSION, THROUGH STABILIZATION OF THE CUMULUS EXTRACELLULAR  
MATRIX THUS SUPPORTING THE PROCESS OF OVULATION.  
RT SUBUNIT: I-ALPHA-1 plasma protease inhibitors are assembled from  
one or two heavy chains (H1, H2 or H3) and one light chain, H2  
and bikunin. Inter-alpha-inhibitor (I-ALPHA-I) is composed of H1, H2  
and bikunin, inter-alpha-like inhibitor (I-ALPHA-LI) of H2 and  
bikunin, and pre-alpha-inhibitor (P-ALPHA-I) of H3 and bikunin (By  
similarity).  
RT PTM: THE PRECURSOR IS PROTEOLYTICALLY PROCESSED INTO TWO  
SEPARATELY FUNCTIONING PROTEINS.  
RT PTM: Alpha-1-microglobulin contains a covalently linked brown-  
yellow chromophore.  
RT SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE LIPOCALIN  
FAMILY.  
RT SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.  
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EMBL; U35642; AAB07599.1;  
PIR; A01209; TIBOBI.  
HSSP; P02760; LBK.  
InterPro; IPR002223; Kunitz\_BPTI.  
InterPro; IPR002345; Lipocalin.  
InterPro; IPR000566; Lipocalin\_cytFABP.  
Pfam; PF00014; Kunitz\_BPTI; 2.  
Pfam; PF00061; lipocalin; 1.  
PRINTS; PR00759; BASICPTASE.  
PRINTS; PR00179; LIPOCALIN.  
SMART; SM00131; K0; 2.  
PROSITE; PS00280; BPTI\_KUNITZ\_1; 2.  
PROSITE; PS0279; BPTI\_KUNITZ\_2; 2.  
PROSITE; PS00213; LIPOCALIN; 1.  
KW Glycoprotein; Plasma; Signal; Serine protease inhibitor; Repeat;  
KW Lipocalin.  
FT SIGNAL 1 19 BY SIMILARITY.  
FT CHAIN 20 303 ALPHA-1 MICROGLOBULIN.  
FT CHAIN 206 352 INTER-ALPHA-TRYPsin INHIBITOR LIGHT  
CHAIN.  
FT DOMAIN 231 281 BPTI/KUNITZ INHIBITOR 1.  
FT DOMAIN 287 337 BPTI/KUNITZ INHIBITOR 2.  
FT BINDING 53 53 CHROMOPHORE (BY SIMILARITY).  
FT DISULFID 91 188 BY SIMILARITY.  
FT DISULFID 231 281 BY SIMILARITY.  
FT DISULFID 240 264 BY SIMILARITY.  
FT DISULFID 256 277 BY SIMILARITY.  
FT DISULFID 287 337 BY SIMILARITY.  
FT DISULFID 296 320 BY SIMILARITY.  
FT DISULFID 312 333 BY SIMILARITY.  
FT ACT\_SITE 241 242 INHIBITORY SITE (PL) (CHYMOTRYPSIN,  
ELASTASE).  
FT ACT\_SITE 297 298 INHIBITORY SITE (PL) (TRYPSIN).  
FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 250 250 N-LINKED (GLCNAC. . .)

FT CONFLICT 209 209 T -> G (IN REF. 4).

FT CONFLICT 217 217 A -> D (IN REF. 4).

FT CONFLICT 268 268 G -> L (IN REF. 2 AND 3).

FT CONFLICT 274 274 E -> Q (IN REF. 2 AND 3).

FT CONFLICT 298 299 SY -> AF (IN REF. 2 AND 3).

FT CONFLICT 330 330 E -> Q (IN REF. 2 AND 3).

FT CONFLICT 346 346 E -> R (IN REF. 2 AND 3).

SQ SEQUENCE 352 AA; 39235 MW; ED31C5CA02E70B19 CRC64;

Query Match 26.3%; Score 249.5; DB 1; Length 352;

Best Local Similarity 32.4%; Pred. No. 1.3e-16;

Matches 48; Conservative 16; Mismatches 45; Indels 39; Gaps 1;

QY 9 DFCVSKVGRCRASPRWYNTDSCQFVYGGDGNNSNYLTKEECLKKCATVTENA 68

DB 229 DSCQDYSGQGLGFKRYNGTSMACETFLYGGCMGNGNLFSEKECLQTCRTV--- 284

QY 69 TGDLATSRNAADSSVPSAPRRDSEHSDMFNYEYCTANAVTGPCRASFPFRWFDVER 128

DB 285 -----EACNLPVQGPCRSYIQLWAFDAVK 309

QY 129 NSCNFNFIYGGCRGNKNSYSEACMLRC 156

DB 310 GKCVRFSGYGGCKGNKGYSEKEKEYC 337

RESULT 7

AMBP\_MERUN STANDARD; PRT; 346 AA.

AC Q62577; Q62576;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE AMBP protein precursor [Contains: Alpha-1-microglobulin; Inter-alpha-

DE trypsin inhibitor light chain (ITI-LC) (Bikunin) (HI-30)].

GN AMBP OR ITIL.

OS Meriones unguiculatus (Mongolian jird).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;

OC Meriones.

OX NCBI\_Taxid=10047;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=95110820; PubMed=7529051;

RA Ide H., Itoh H., Nawa Y.;

RT "Sequencing of cDNAs encoding alpha 1-microglobulin/bikunin of

RT Mongolian gerbil and Syrian golden hamster in comparison with man and

RT other species.";

RL Biochim. Biophys. Acta 1209:286-292(1994).

CC -!- FUNCTION: ALPHA-1-MICROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL

CC FLUIDS INCLUDING PLASMA, URINE, AND CEREBROSPINAL FLUID. IT

CC APPEARS NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH IGA

CC AND ALBUMIN (BY SIMILARITY).

CC -!- FUNCTION: INTER-ALPHA-TRYPsin INHIBITOR, PRESENT IN PLASMA AND

CC URINE, INHIBITS TRYPSIN, PLASMIN, AND LYSOSOMAL GRANULOCYTIC

CC ELASTASE (BY SIMILARITY).

CC -!- SUBUNIT: 1-ALPHA-I plasma protease inhibitors are assembled from

CC one or two heavy chains (H1, H2 or H3) and one light chain,

CC bikunin. Inter-alpha-inhibitor (I-ALPHA-I) is composed of H1, H2

CC and bikunin, inter-alpha-like inhibitor (I-ALPHA-LI) of H2 and

CC bikunin, and pre-alpha-inhibitor (P-ALPHA-I) of H3 and bikunin (By

CC similarity).

CC -!- PTM: THE PRECURSOR IS PROTEOLYTICALLY PROCESSED INTO TWO

CC SEPARATELY FUNCTIONING PROTEINS.

CC -!- PTM: Alpha-1-microglobulin contains a covalently linked brown-

CC yellow chromophore (By similarity).

CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE LIPOCALIN

CC FAMILY.

CC -!- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.

CC

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CC -----

DR EMBL; D31813; BAA06600.1; -.

DR HSSP; P02760; 1BJK.

DR InterPro; IPR002223; Kunitz\_BPTI.

DR InterPro; IPR002345; Lipocalin.

DR InterPro; IPR000566; Lipocln\_cytFABP.

DR Pfam; PF00014; Kunitz\_BPTI; 2.

DR Pfam; PF00061; Lipocalin; 1.

DR PRINTS; PR00759; BASICPTASE.

DR PRINTS; PR00179; LIPOCALIN.

DR SMART; SM00131; KU; 2.

DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 2.

DR PROSITE; PS00279; BPTI\_KUNITZ\_2; 2.

KW Glycoprotein; Plasma; Signal; Serine protease inhibitor; Repeat;

KW Lipocalin.

FT SIGNAL 1 19 BY SIMILARITY.

FT CHAIN 20 202 ALPHA-1 MICROGLOBULIN.

FT CHAIN 205 346 INTER-ALPHA-TRYPSIN INHIBITOR LIGHT

FT CHAIN 205 346 CHAIN.

FT DOMAIN 230 280 BPTI/KUNITZ INHIBITOR 1.

FT DOMAIN 286 336 BPTI/KUNITZ INHIBITOR 2.

FT BINDING 52 52 CHROMOPHORE (BY SIMILARITY).

FT DISULFID 90 187 BY SIMILARITY.

FT DISULFID 230 280 BY SIMILARITY.

FT DISULFID 239 263 BY SIMILARITY.

FT DISULFID 255 276 BY SIMILARITY.

FT DISULFID 286 336 BY SIMILARITY.

FT DISULFID 295 319 BY SIMILARITY.

FT DISULFID 311 332 BY SIMILARITY.

FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT ACT\_SITE 240 241 INHIBITORY SITE (P1) (CHYMOTRYPSIN,

FT ACT\_SITE 296 297 ELASTASE) (BY SIMILARITY).

FT ACT\_SITE 296 297 INHIBITORY SITE (P1) (TRYPSIN) (BY

FT ACT\_SITE 296 297 SIMILARITY).

SQ SEQUENCE 346 AA; 38643 MW; FIA463810918D5F CRC64;

Query Match 26.1%; Score 247.5; DB 1; Length 346;

Best Local Similarity 32.4%; Pred. No. 2e-16;

Matches 48; Conservative 15; Mismatches 46; Indels 39; Gaps 1;

QY 9 DFCVSKVGRCRASPRWYNTDSCQFVYGGDGNNSNYLTKEECLKKCATVTENA 68

DB 228 DSCQDYSGQGLGFKRYNGTSMACETFOYGGCLGNGNFISEKECLQTCRTVAA-- 285

QY 69 TGDLATSRNAADSSVPSAPRRDSEHSDMFNYEYCTANAVTGPCRASFPFRWFDVER 128

DB 286 -----CNLPVQGPCRAYIKLWAFDAQ 308

QY 129 NSCNFNFIYGGCRGNKNSYSEACMLRC 156

DB 309 GKCIQFTYGGCKGNKGYSEKEKEYC 336

RESULT 8

TFPI\_RAT STANDARD; PRT; 302 AA.

ID TFPI\_RAT

AC Q02445;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Tissue factor pathway inhibitor precursor (TFPI) (Lipoprotein-

DE associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)

DE (EPI).

GN TFPI.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

Dd	182	QKGDYVNTQTIVTDRTVNNVVTPOATKAPSQWDYDGP-----WCLEPADSLCKA
Qy	118	SFRWFDFVNSCNFIYGCGRGNKNYSREACMLRC 156 I I L I I I I I I I : : I I
Dd	234	SEKFYINPAIGCRQFNFTGCGGNNNFTTKDCNRC 272
RESULT 9		
ID	IATR_SHEEP	STANDARD; PRT; 123 AA.
AC	P13371;	
DT	01-JAN-1990 (Rel. 13, Created)	
DT	01-JAN-1990 (Rel. 13, Last sequence update)	
DT	16-OCT-2001 (Rel. 40, Last annotation update)	
DE	Inter-alpha-trypsin inhibitor (ITI) (GIK-14) (Inhibitory fragment of ITI) (Fragment).	
DE	Ovis aries (Sheep), and	
OS	Capra hircus (Goat).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;	
OC	Bovidae; Caprinae; Ovis.	
OX	NCBI_TaxID=9940, 9925;	
RN	[1]	
RP	SEQUENCE.	
RC	SPECIES=Sheep;	
RX	MEDLINE=87299012; PubMed=2441725;	
RA	Rasp G., Hochstrasser K., Wachter E., Reisinger P.W.M.;	
RT	"The amino-acid sequence of the trypsin-released inhibitor from sheep inter-alpha-trypsin inhibitor."	
RL	Biol. Chem. Hoppe-Seyler 368:727-731(1987). [2]	
RN	SEQUENCE.	
RC	SPECIES=C.hircus;	
RX	MEDLINE=90105540; PubMed=2481505;	
RA	Rasp G., Hochstrasser K., Gerl C., Wachter E.;	
RT	"Primary structure of a proteinase inhibitor released from goat serum inter-alpha-trypsin inhibitor.";	
RL	Biochim. Biophys. Acta 999:335-337(1989).	
CC -1-	FUNCTION: THIS INHIBITORY FRAGMENT, RELEASED FROM NATIVE ITI AFTER LIMITED PROTEOLYSIS WITH TRYPSIN, CONTAINS TWO HOMOLOGOUS DOMAINS WHEREAS THE SECOND DOMAIN IS A STRONG INHIBITOR OF TRYP SIN, THE FIRST DOMAIN INTERACTS WEAKLY WITH PMN-GRANULOCYTIC ELASTASE AND NOT AT ALL WITH PANCREATIC ELASTASE.	
CC -1-	MISCELLANEOUS: THE AMINO ACID AT POSITION P2' (17) APPEARS TO DETERMINE THE SPECIFICITY OF THE INHIBITION OF DOMAIN 1.	
CC	INHIBITORS WITH METHIONINE IN THIS POSITION INTERACT WEAKLY WITH CHYMOTRYPSIN AND ELASTASE; THOSE WITH LEUCINE INTERACT STRONGLY.	
CC -1-	SIMILARITY: CONTAINS 2 BP TI/KUNITZ INHIBITOR DOMAINS. PIR; A29652; A29652. HSSP; P02760; 1B1K.	
DR	InterPro: IPR002223; Kunitz_BP TI.	
DR	pfam: PF00014; Kunitz_BP TI; 2.	
DR	SMART: SM00131; KU; 2.	
DR	PROSITE: PS00280; BP TI_KUNITZ_1; 2.	
DR	PROSITE: PS50279; BP TI_KUNITZ_2; 2.	
KW	Plasma; Glycoprotein; Serine protease inhibitor; Repeat.	
FT NON_TER	1	
FT DOMAIN	5 55	BPTI/KUNITZ INHIBITOR 1.
FT DOMAIN	61 111	BPTI/KUNITZ INHIBITOR 2.
FT DISULFID	5 55	BY SIMILARITY.
FT DISULFID	14 38	BY SIMILARITY.
FT DISULFID	30 51	BY SIMILARITY.
FT DISULFID	61 111	BY SIMILARITY.
FT DISULFID	70 94	BY SIMILARITY.
FT DISULFID	86 107	BY SIMILARITY.
FT ACT_SITE	15 16	INHIBITORY SITE (P1) (CHYMOTRYPSIN, ELASTASE).
FT ACT_SITE	71 72	INHIBITORY SITE (P1) (TRYPSIN).
FT CARBOHYD	24 24	N-LINKED (GLCNAc...).
FT NON_TER	123 123	
SEQ SEQUENCE	123 AA; 13686 MW; 295038173F22D2DI CRC64;	
Query Match	25.8%; Score 244.5; DB 1; Length 123;	





RT blood protein pre-alpha-inhibitor.";  
 RL J. Biol. Chem. 266:747-751(1991).  
 RN [16]  
 RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 230-339.  
 RA MEDLINE=98227321; PubMed=9566199;  
 RA Xu Y., Carr P.D., Guss J.M., Ollis D.L.;  
 RT "The crystal structure of bikunin from the inter-alpha-inhibitor  
 complex: a serine protease inhibitor with two Kunitz domains.";  
 RL J. Mol. Biol. 276:955-966(1998).  
 CC -!- FUNCTION: ALPHA-1-MICROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL  
 CC FLUIDS INCLUDING PLASMA, URINE, AND CEREBROSPINAL FLUID. IT  
 CC APPEARS NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH IGA  
 CC AND ALBUMIN.  
 CC -!- FUNCTION: INTER-ALPHA-TRYPsin INHIBITOR, PRESENT IN PLASMA AND  
 CC URINE, INHIBITS TRYPSIN, PLASMIN, AND LYSOSOMAL GRANULOCYTIC  
 CC ELASTASE. ADDITIONAL PROTEOLYTIC PROCESSING IN THE KIDNEY AND/OR  
 CC URINE CAN PRODUCE FURTHER AMINO- AND CARBOXYL-END MODIFICATIONS  
 CC IN ITS SEQUENCE.  
 CC -!- SUBUNIT: I-ALPHA-I plasma protease inhibitors are assembled from  
 CC one or two heavy chains (H1, H2 or H3) and one light chain,  
 CC bikunin. Inter-alpha-inhibitor (I-ALPHA-I) is composed of H1, H2  
 CC and bikunin, inter-alpha-like inhibitor (I-ALPHA-LI) of H2 and  
 CC bikunin, and pre-alpha-inhibitor (P-ALPHA-I) of H3 and bikunin (by  
 CC similarity).  
 CC -!- PTM: THE PRECURSOR IS PROTEOLYTICALLY PROCESSED INTO TWO  
 CC SEPARATELY FUNCTIONING PROTEINS.  
 CC -!- PTM: Alpha-1-microglobulin contains a covalently linked brown-  
 CC yellow chromophore.  
 CC -!- PTM: ADDITION OF GLYCOSAMINOGLYCAN CHONDROITIN SULFATE, ALLOWS  
 CC CROSS-LINKING BETWEEN THE DIFFERENT COMPONENTS.  
 CC -!- MISCELLANEOUS: IN VITRO, THE FIRST TWELVE RESIDUES OF THE AMINO  
 CC END OF THE INHIBITOR APPEAR TO HAVE A REACTIVE SITE CAPABLE OF  
 CC INHIBITING THE ACTIVITY OF A NUMBER OF ENZYMES. ITS IN VIVO  
 CC FUNCTION IS NOT KNOWN.  
 CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE LIPOCALIN  
 CC FAMILY.  
 CC -!- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; X54816; CAA38585.1; JOINED.  
 DR EMBL; X54817; CAA38585.1; JOINED.  
 DR EMBL; X54818; CAA38585.1; JOINED.  
 DR EMBL; X04225; CAA27803.1; -.  
 DR EMBL; M88249; AAA59196.1; -.  
 DR EMBL; M88165; AAA59196.1; JOINED.  
 DR EMBL; M88243; AAA59196.1; JOINED.  
 DR EMBL; M88244; AAA59196.1; JOINED.  
 DR EMBL; M88246; AAA59196.1; JOINED.  
 DR EMBL; M88247; AAA59196.1; JOINED.  
 DR EMBL; X04494; CAA28182.1; -.  
 DR EMBL; X54817; CAA38586.1; -.  
 DR PIR; A03217; HCHU  
 DR PIR; A25303; A25303.  
 DR PIR; S13433; S13433.  
 DR PIR; S10717; S10717.  
 DR PDB; 1BIK; 16-MAR-99.  
 DR GlycosuitedB; P02760; -.  
 DR SWISS-2DPAGE; P02760; HUMAN.  
 DR Siena-2DPAGE; P02760; -.  
 DR MIM; I76870; -.  
 DR InterPro; IPR002223; Kunitz\_BPTI.  
 DR InterPro; IPR002345; Lipocalin.  
 DR InterPro; IPR000566; Lipocalin\_cytfabp.  
 DR Pfam; PF00014; Kunitz\_BPTI; 2.  
 DR Pfam; PF00061; Lipocalin; 1.

Query Match 25.8%; Score 244.5; DB 1; Length 352;  
 Best Local Similarity 32.4%; Pred. No. 4e-16;  
 Matches 48; Conservative 14; Mismatches 47; Indels 39; Gaps 1;  
 QY 9 DCLVSKVVGRCRASPRWYVNTDSCQLFVYGGCDGNSNNLYLKECLKKCAVTYENA 68  
 DB 229 DSCQLGYSAGPCMGMTSRFYNGTSMACETFOYGGCMGNNFVTEKECLQTCRTVAA-- 286  
 QY 69 TGDLSATRNAADSSVPSAPRRQDSHSDMFENYECYANAVTGPCRASFPFWYFDVER 128  
 DB 287 -----CNLPVIRGCPRAFIQLWAFDAVK 309  
 QY 129 NSCNNFIYGGCRGNKNSYRSEECMLRC 156  
 DB 310 GKCVLPYGGCGNGNKFYSEKREYVC 337  
 RESULT 11  
 TFPI\_RABBIT STANDARD; PRT; 300 AA.  
 AC P19761; Q28828;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Tissue factor pathway inhibitor precursor (TFPI) (lipoprotein-  
 DE associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)  
 DE (EPI).  
 GN TFPI.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=91057146; PubMed=2136251;  
 RA Wesselschmidt R.L., Girard T.J., Broze G.J. Jr.;  
 RT "cDNA sequence of rabbit lipoprotein-associated coagulation  
 RT inhibitor.";  
 RL Nucleic Acids Res. 18:6440-6440(1990).  
 RN [2]  
 RP REVISIONS TO 72; 211 AND 218.  
 RC TISSUE=Liver;  
 RX MEDLINE=92335027; PubMed=1630940;  
 RA Warn-Cramer B.J., Broze G.J. Jr., Komives E.A.;  
 RT "cDNA sequence of rabbit tissue factor pathway inhibitor.";  
 RL Nucleic Acids Res. 20:3548-3548(1992).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=93276427; PubMed=8503123;  
 RA Belaaouaj A., Kuppaswamy M.N., Birktoft J.J., Bajaj S.P.;  
 RT "Revised cDNA sequence of rabbit tissue factor pathway inhibitor.";  
 RL Thromb. Res. 69:547-553(1993).  
 CC -!- FUNCTION: INHIBITS FACTOR X (X(A)) DIRECTLY AND, IN A XA-DEPENDENT  
 CC WAY, INHIBITS VII(A)/TISSUE FACTOR ACTIVITY, PRESUMABLY BY FORMING  
 CC A QUATERNARY X(A)/LACI/VII(A)/TF COMPLEX. IT POSSESSES AN  
 CC ANTITHROMBOTIC ACTION AND ALSO THE ABILITY TO ASSOCIATE WITH  
 CC LIPOPROTEINS IN PLASMA.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.  
 CC -!- SIMILARITY: CONTAINS 3 BPTI/KUNITZ INHIBITOR DOMAINS.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; X54708; CAA38515.1; ALT\_SEQ.  
 DR EMBL; S61902; AAB26836.1; -.

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DR PIR; S12143; S12143.
DR HSSP; P10646; 1TFX.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 3.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 3.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 3.
KW Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation;
KW Signal.
FT SIGNAL. 1 24
FT CHAIN 25 300
FT DOMAIN 50 100
FT
FT DOMAIN 121 171
FT
FT DOMAIN 213 263
FT
FT DISULFID 50 100
FT DISULFID 59 83
FT DISULFID 75 96
FT ACT_SITE 60 61
FT DISULFID 121 171
FT DISULFID 130 154
FT DISULFID 146 167
FT ACT_SITE 131 132
FT DISULFID 213 263
FT DISULFID 222 246
FT DISULFID 238 259
FT ACT_SITE 223 224
FT CARBOHYD 141 141
FT CARBOHYD 191 191
FT CARBOHYD 252 252
FT CONFLICT 31 31
FT CONFLICT 269 272
FT CONFLICT 300 AA; 34435 MW; A08DE36537708CA6 CRC64;
SQ SEQUENCE 300 AA; 34435 MW; A08DE36537708CA6 CRC64;

Query Match 25.7%; Score 244; DB 1; Length 300;
Best Local Similarity 30.0%; Pred No. 3.7e-16;
Matches 48; Conservative 23; Mismatches 61; Indels 28; Gaps 2;

QY 4 ERSIHDFCLVSKVVGRCASMPRWVNTDGSQFLVYGGDGNSSNNYLTKEELKKCAT 63
Db 43 QKPTSFCAKVDGDCRAYIKRFFENILTHOCEEIYGGCEGNENRFESLECKEKAR 102
QY 64 VTENATGDLATSNADSSVPSAPRQDSEHDHSSDMFNEEYCTANAVTGPCRASEPPRY 123
Db 103 DYPKMTTKLTFOKQKPD-----FCFLEEDPGICRGYITRYF 138
QY 124 FVDERNSCNFIYGGRCGRNKNYSRSEACMLRCFRQOENP 163
Db 139 YNNQSKQCFERFYGGCLGNLNFESLECKNTC-----ENP 174

RESULT 12
AMBP.PIG
ID AMBP_PIG STANDARD; PRT; 337 AA.
AC P04366; P34954;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE AMBP protein precursor [Contains: Alpha-1-microglobulin; Inter-alpha-
DE trypsin inhibitor light chain (ITI-LC) (Bikunin) (HI-30) (EI-14)]
DE (Fragment).
GN AMBP OR ITIL.
OS Sus scrofa (Pig).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
[1]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=90353595; PubMed=1696914;
RA Gebhard W., Schreitmuller T., Vetr H., Wachter E., Hochstrasser K.;

"Complementary DNA and deduced amino acid sequences of porcine alpha
1-microglobulin and bikunin.";
FEBS Lett. 269:32-36(1990).
[2]
SEQUENCE OF 2-337 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91113729; PubMed=1703444;
RA Tavakkol A.;
FT "Molecular cloning of porcine alpha 1-microglobulin/HI-30 reveals
FT developmental and tissue-specific expression of two variant messenger
FT ribonucleic acids.";
RL Biochim. Biophys. Acta 1088:47-56(1991).
[3]
SEQUENCE OF 212-334.
RX MEDLINE=85225967; PubMed=2408637;
RA Hochstrasser K., Wachter E., Albrecht G.J., Reisinger P.;
FT "Kunitz-type proteinase inhibitors derived by limited proteolysis of
FT the inter-alpha-trypsin inhibitor, X. The amino-acid sequences of the
FT trypsin-released inhibitors from horse and pig inter-alpha-trypsin
FT inhibitors.";
RL Biol. Chem. Hoppe-Seyler 366:473-478(1985).
CC -!- FUNCTION: ALPHA-1-MICROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL
CC FLUIDS INCLUDING PLASMA, URINE, AND CEREBROSPINAL FLUID. IT
CC APPEARS NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH IGA
CC AND ALBUMIN.
CC -!- FUNCTION: INTER-ALPHA-TRYPsin INHIBITOR, PRESENT IN PLASMA AND
CC URINE. INHIBITS TRYPSIN, PLASMIN, AND LYSOSOMAL GRANULOCYTIC
CC ELASTASE.
CC -!- SUBUNIT: I-ALPHA-I plasma protease inhibitors are assembled from
CC one or two heavy chains (H1, H2 or H3) and one light chain,
CC bikunin. Inter-alpha-inhibitor (I-ALPHA-I) is composed of H1, H2
CC and bikunin, inter-alpha-like inhibitor (I-ALPHA-LI) of H2 and
CC bikunin, and pre-alpha-inhibitor (P-ALPHA-I) of H3 and bikunin (By
CC similarity).
CC -!- PTM: THE PRECURSOR IS PROTEOLYTICALLY PROCESSED INTO TWO
CC SEPARATELY FUNCTIONING PROTEINS.
CC -!- PTM: Alpha-1-microglobulin contains a covalently linked brown-
CC yellow chromophore.
CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE LIPOCALIN
CC FAMILY.
CC -!- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.
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or send an email to license@isb-sib.ch).
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EMBL; X53685; CAA37725.1; -.
DR EMBL; X52087; CAA36306.1; -.
DR PIR; A01208; TIPGB1.
DR PIR; S11066; S11066.
DR HSSP; P02760; IBIK.
DR InterPro; IPR002223; Kunitz_BPTI.
DR InterPro; IPR000566; Lipocln_cytfabp.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00061; lipocalin; 1.
DR SMART; SM00131; KU; 2.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00213; LIPOCALIN; 1.
KW Glycoprotein; Plasma; Signal; Serine protease inhibitor; Repeat;
KW Lipocalin.
FT NON_TER 1 1
FT SIGNAL <1 4
FT CHAIN 5 188
FT CHAIN 191 337
FT
FT DOMAIN 216 266
FT DOMAIN 272 322
FT BINDING 38 38
BY SIMILARITY.
ALPHA-1-MICROGLOBULIN.
INTER-ALPHA-TRYPSIN INHIBITOR LIGHT
CHAIN.
BPTI/KUNITZ INHIBITOR 1.
BPTI/KUNITZ INHIBITOR 2.
CHROMOPHORE (BY SIMILARITY).
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FT DISULFID 76 173 BY SIMILARITY.  
FT DISULFID 216 266  
FT DISULFID 225 249  
FT DISULFID 241 262  
FT DISULFID 272 322  
FT DISULFID 281 305  
FT DISULFID 297 318  
FT DISULFID 100 100  
FT CARBOHYD 235 235  
FT ACT\_SITE 226 227  
FT ACT\_SITE 282 283  
FT CONFLICT 49 49  
FT CONFLICT 259 259  
FT CONFLICT 270 270  
FT CONFLICT 278 278  
FT CONFLICT 283 283  
FT CONFLICT 285 286  
FT CONFLICT 293 293  
FT CONFLICT 311 311  
FT CONFLICT 315 315  
SQ SEQUENCE 337 AA; 37690 MW; 1F630FF98B3CD70F CRC64;  
  
Query Match 25.6%; Score 242.5; DB 1; Length 337;  
Best Local Similarity 31.8%; Pred. No. 5.9e-16;  
Matches 47; Conservative 19; Mismatches 43; Indels 39; Gaps 1;  
  
QY 9 DFCVSKVYGRGRASPRWYNTDSCOLFVYGGDGNNSNYLTKKECLKKCATVTENA 68  
DB 214 DSCQGYSGPCGLMIRFYNGSSMACETFFHYGGMGNGNFVSEKELQCTRTV--- 269  
QY 69 TGDLATSRNAADSSVPSAPRRQDSEHSDMFENYECYCTANAVTGPCRASFPFRWYFDVER 128  
DB 270 -----EACSLPIVSGPCRGFFQLWAFDAVQ 294  
QY 129 NSCNFIYGGCRGNKNSYRSEACMLRC 156  
DB 295 GKCVLFYGGCGNGNQFYSEKEKEYC 322  
  
RESULT 13  
IATR\_HORSE  
ID IATR\_HORSE STANDARD; PRT; 123 AA.  
AC P04365;  
DT 20-MAR-1987 (Rel. 04, Created)  
DT 20-MAR-1987 (Rel. 04, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Inter-alpha-trypsin inhibitor (ITI) (HI-14) (Inhibitory fragment of  
DE .ITI) (fragment).  
OS Equus caballus (Horse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_TaxID=9796;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=85225967; PubMed=2408637;  
RA Hochstrasser K., Wachter E., Albrecht G.J., Reisinger P.;  
RT "Kunitz-type proteinase inhibitors derived by limited proteolysis of  
RT the inter-alpha-trypsin inhibitor, X. The amino-acid sequences of the  
RT trypsin-released inhibitors from horse and pig inter-alpha-trypsin  
RT inhibitors.";  
RL Biol. Chem. Hoppe-Seyler 366:473-478(1985).  
CC -!- FUNCTION: THIS INHIBITORY FRAGMENT, RELEASED FROM NATIVE ITI AFTER  
CC LIMITED PROTEOLYSIS WITH TRYPSIN, CONTAINS TWO HOMOLOGOUS DOMAINS.  
CC WHEREAS THE SECOND DOMAIN IS A STRONG INHIBITOR OF TRYPSIN, THE  
CC FIRST DOMAIN INTERACTS WEAKLY WITH PMN-GRANULOCYTIC ELASTASE AND  
CC NOT AT ALL WITH PANCREATIC ELASTASE.  
CC DETERMINE THE SPECIFICITY OF THE INHIBITION OF DOMAIN I.  
CC INHIBITORS WITH METHIONINE IN THIS POSITION INTERACT WEAKLY WITH  
CC CHYMOTRYPSIN AND ELASTASE; THOSE WITH LEUCINE INTERACT STRONGLY.  
CC -!- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.  
DR PIR; A01210; TIH01.

DR HSP; P02760; IBIK.  
DR InterPro; IPR002223; Kunitz\_BPTI.  
DR Pfam; PF00014; Kunitz\_BPTI; 2.  
DR SMART; SM00131; KU; 2.  
DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 2.  
DR PROSITE; PS00279; BPTI\_KUNITZ\_2; 2.  
KW Plasma; Glycoprotein; Serine protease inhibitor; Repeat.  
FT NON\_TER 1 1  
FT DOMAIN 5 55 BPTI/KUNITZ INHIBITOR 1.  
FT DOMAIN 61 111 BPTI/KUNITZ INHIBITOR 2.  
FT DISULFID 5 55  
FT DISULFID 14 38  
FT DISULFID 30 51  
FT DISULFID 61 111  
FT DISULFID 70 94  
FT DISULFID 86 107  
FT ACT\_SITE 15 16 INHIBITORY SITE (P1) (CHYMOTRYPSIN,  
FT ELASTASE).  
FT ACT\_SITE 71 72 INHIBITORY SITE (P1) (TRYPSIN).  
FT CARBOHYD 24 24 N-LINKED (GLCNAC. .).  
FT NON\_TER 123 123  
SQ SEQUENCE 123 AA; 13510 MW; CEIA9120774411D5 CRC64;  
  
Query Match 25.5%; Score 241.5; DB 1; Length 123;  
Best Local Similarity 31.8%; Pred. No. 2.4e-16;  
Matches 47; Conservative 15; Mismatches 47; Indels 39; Gaps 1;  
  
QY 9 DFCVSKVYGRGRASPRWYNTDSCOLFVYGGDGNNSNYLTKKECLKKCATVTENA 68  
DB 3 DSCQDHAQGCPLGIMISRYFYNGTSMACETFFYGGCLNGNPFASQKECLQCTRTVAA-- 60  
QY 69 TGDLATSRNAADSSVPSAPRRQDSEHSDMFENYECYCTANAVTGPCRASFPFRWYFDVER 128  
DB 61 -----CNLPIVQGPCRAFIRLWAFDAQAQ 83  
QY 129 NSCNFIYGGCRGNKNSYRSEACMLRC 156  
DB 84 GKCVLFYGGCRGNKNSYRSEACMLRC 111  
  
RESULT 14  
AMBP\_RAT  
ID AMBP\_RAT STANDARD; PRT; 349 AA.  
AC Q64240; Q63336; P19603;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE AMBP protein precursor [Contains: Alpha-1-microglobulin; Inter-alpha-  
DE trypsin inhibitor light chain (ITI-LC) (Bikunin) (HI-30); Trypsin].  
GN AMBP OR ITIL.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Liver;  
RX MEDLINE=92182014; PubMed=1371936;  
RA Lindqvist A., Bratt T., Altieri M., Kastern W., Akerstrom B.;  
RT "Rat alpha 1-microglobulin: co-expression in liver with the light  
RT chain of inter-alpha-trypsin inhibitor.";  
RL Biochim. Biophys. Acta 1130:63-67(1992).  
RN [2]  
RP SEQUENCE OF 141-195 FROM N.A.  
RX MEDLINE=87033744; PubMed=2429963;  
RA Kastern W., Bjoerck L., Akerstrom B.;  
RT "Developmental and tissue-specific expression of alpha 1-microglobulin  
RT mRNA in the rat.";  
RL J. Biol. Chem. 261:15070-15074(1986).  
RN [3]  
RP SEQUENCE OF 283-343, AND CHARACTERIZATION.  
RC STRAIN-WISTAR;  
RX MEDLINE=89053978; PubMed=3263966;

RA Kido H., Yokogoshi Y., Katunuma N.;  
 RT "Kunitz-type protease inhibitor found in rat mast cells. Purification,  
 properties, and amino acid sequence.";  
 RL J. Biol. Chem. 263:18104-18107(1988).  
 RN [4]  
 RP PROCESSING.  
 RX MEDLINE=94148892; PubMed=7508921;  
 RA Itoh H., Ide H., Ishikawa N., Nawa Y.;  
 RT "Mast cell protease inhibitor, trypstatin, is a fragment of  
 inter-alpha-trypsin inhibitor light chain.";  
 RL J. Biol. Chem. 269:3818-3822(1994).  
 CC -!- FUNCTION: ALPHA-1-MICROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL  
 CC FLUIDS INCLUDING PLASMA, URINE, AND CEREBROSPINAL FLUID. IT  
 CC APPEARS NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH IGA  
 CC AND ALBUMIN (BY SIMILARITY).  
 CC -!- FUNCTION: INTER-ALPHA-TRYPsin INHIBITOR, PRESENT IN PLASMA AND  
 CC URINE, INHIBITS TRYPSIN, PLASMIN, AND LYSOSOMAL GRANULOCYTIC  
 CC ELASTASE (BY SIMILARITY).  
 CC -!- FUNCTION: Trypstatin is a trypsin inhibitor. It inhibits blood  
 CC coagulation factor Xa and trypsinase about 100-fold more rapidly  
 CC than porcine pancreatic trypsin and chymase. It is a monomer but  
 CC is also found in mast cells as a complex with tryptase.  
 CC -!- SUBUNIT: I-ALPHA-1 plasma protease inhibitors are assembled from  
 CC one or two heavy chains (H1, H2 or H3) and one light chain,  
 CC bikunin. Inter-alpha-inhibitor (I-ALPHA-I) is composed of H1, H2  
 CC and bikunin, inter-alpha-like inhibitor (I-ALPHA-LI) of H2 and  
 CC bikunin, and pre-alpha-inhibitor (P-ALPHA-I) of H3 and bikunin (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Trypstatin is present in mast cell granules.  
 CC -!- PTM: The precursor is proteolytically processed into separately  
 CC functioning proteins.  
 CC -!- PTM: Alpha-1-microglobulin contains a covalently linked brown-  
 CC yellow chromophore (By similarity).  
 CC -!- PTM: Heavy chains are interlinked with bikunin via a chondroitin  
 CC 4-sulfate bridge to the their C-terminal aspartate (By  
 CC similarity).  
 CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE LIPOCALIN  
 CC FAMILY.  
 CC -!- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.  
 CC  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC  
 CC EMBL; S87544; AAB21782.1; -;  
 CC EMBL; J02600; AAA41596.1; -;  
 CC PIR; A31890; A31890.  
 CC HSP; P02760; LB1K.  
 CC InterPro; IPR002223; Kunitz\_BPTI.  
 CC InterPro; IPR002345; Lipocalin.  
 CC InterPro; IPR000566; Lipocalin\_cytfabp.  
 CC Pfam; PF00014; Kunitz\_BPTI; 2.  
 CC Pfam; PF00061; Lipocalin; 1.  
 CC PRINTS; PR00759; BASICPTASE.  
 CC PRINTS; PR001179; LIPOCALIN.  
 CC SMART; SM00131; KD; 2.  
 CC PROSITE; PS00280; BPTI\_KUNITZ\_1; 2.  
 CC PROSITE; PS00279; BPTI\_KUNITZ\_2; 2.  
 CC PROSITE; PS00213; LIPOCALIN; 1.  
 CC Glycoprotein; Plasma; Signal; Serine protease inhibitor; Repeat;  
 KW Lipocalin.  
 FT SIGNAL 1 19 BY SIMILARITY.  
 FT CHAIN 20 202 ALPHA-1-MICROGLOBULIN.  
 FT CHAIN 205 349 INTER-ALPHA-TRYPsin INHIBITOR LIGHT  
 FT CHAIN  
 FT CHAIN 283 343 TRYPSATIN.  
 FT DOMAIN 230 280 BPTI/KUNITZ INHIBITOR 1.  
 FT DOMAIN 286 336 BPTI/KUNITZ INHIBITOR 2.  
 FT BINDING 52 52 CHROMOPHORE (BY SIMILARITY).  
 FT

FT DISULFID 90 187 BY SIMILARITY.  
 FT DISULFID 230 280 BY SIMILARITY.  
 FT DISULFID 239 263 BY SIMILARITY.  
 FT DISULFID 255 276 BY SIMILARITY.  
 FT DISULFID 286 336 BY SIMILARITY.  
 FT DISULFID 295 319 BY SIMILARITY.  
 FT DISULFID 311 332 BY SIMILARITY.  
 FT CARBOHYD 114 114 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 233 233 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT ACT\_SITE 240 241 INHIBITORY SITE (PI) (CHYMOTRYPSIN,  
 FT ELASTASE) (BY SIMILARITY).  
 FT ACT\_SITE 296 297 INHIBITORY SITE (PI) (TRYPSIN) (BY  
 FT SIMILARITY).  
 FT CONFLICT 142 142 G -> A (IN REF. 2).  
 FT CONFLICT 302 302 W -> L (IN REF. 3).  
 FT CONFLICT 323 323 G -> N (IN REF. 3).  
 FT CONFLICT 330 331 KE -> PK (IN REF. 3).  
 FT CONFLICT 334 334 E -> W (IN REF. 3).  
 SQ SEQUENCE 349 AA; 38851 MW; 1B7FB7DCB0824E01 CRC64;  
 Query Match 25.1%; Score 237.5; DB 1; Length 349;  
 Best Local Similarity 30.4%; Pred. No. 1.8e-15;  
 Matches 45; Conservative 17; Mismatches 47; Indels 39; Gaps 1;  
 QY 9 DFCLVSKVYVGRASMPRWNVDTGSCOLFVYGGDGNNSNYLTKECKKKCATVVTENA 68  
 DB 228 DSCOLNYSSEGPCLGQQKYYNGASMACETFOYGGCLGNGNFASEKECLOTCRTIAA-- 285  
 QY 69 TGDLTATRNAADSSVPSAPRRDSDHSDSMENYEEYCTANAVTGPCRASFPWFYDVER 128  
 DB 286 -----CNLPVVGPCRAFAELWAFDAQAQ 308  
 QY 129 NSCNFNFIYGGCRGNKNSYSEACMLRC 156  
 DB 309 GKCIQFIYGGCKGNKIFYSECKEYIC 336  
 RESULT 15  
 TFPI\_MACMU STANDARD; PRT; 304 AA.  
 AC Q28864;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Tissue factor pathway inhibitor precursor (TFPI) (Lipoprotein-  
 DE associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)  
 DE (EPI).  
 GN TFPI OR TFPII.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver.  
 RX MEDLINE=94375417; PubMed=8089087;  
 RA Kamei S., Kamikubo Y., Hamuro T., Fujimoto H., Ishihara M.,  
 RA Ionomura H., Miyamoto S., Funatsu A., Enyoji K., Abumiya T.;  
 RT "Amino acid sequence and inhibitory activity of rhesus monkey tissue  
 RT factor pathway inhibitor (TFPI): comparison with human TFPI.";  
 RL J. Biochem. 115:708-714(1994).  
 CC -!- FUNCTION: INHIBITS FACTOR X (X(A)) DIRECTLY AND, IN A XA-DEPENDENT  
 CC WAY, INHIBITS VII(A)/TISSUE FACTOR ACTIVITY, PRESUMABLY BY FORMING  
 CC A QUATERNARY X(A)/LACI/VII(A)/TF COMPLEX. IT POSSESSES AN  
 CC ANTITHROMBOTIC ACTION AND ALSO THE ABILITY TO ASSOCIATE WITH  
 CC LIPOPROTEINS IN PLASMA.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.  
 CC -!- PTM: O-GLYCOSYLATED (BY SIMILARITY).  
 CC -!- SIMILARITY: CONTAINS 3 BPTI/KUNITZ INHIBITOR DOMAINS.  
 CC  
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-----  
 DR EMBL; S73337; AAB31955.1; -  
 DR HSP; P10646; ITFX.  
 DR InterPro; IPR002223; Kunitz\_BPTI.  
 DR Pfam; PF00014; Kunitz\_BPTI; 3.  
 DR PRINTS; PR00759; BASICTPASE.  
 DR SMART; SM00131; KU; 3.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 3.  
 DR PROSITE; PS0279; BPTI\_KUNITZ\_2; 3.  
 KW Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation;  
 KW Signal.  
 FT SIGNAL 1 28 BY SIMILARITY.  
 FT CHAIN 29 304 TISSUE FACTOR PATHWAY INHIBITOR.  
 FT DOMAIN 54 104 BPTI/KUNITZ INHIBITOR 1  
 FT (VII(A)/TISSUE FACTOR BINDING SITE).  
 FT BPTI/KUNITZ INHIBITOR 2  
 FT BPTI/KUNITZ INHIBITOR 3.  
 FT (FACTOR X(A) BINDING SITE).  
 FT BPTI/KUNITZ INHIBITOR 3.  
 FT BY SIMILARITY.  
 FT DISULFID 54 104 BY SIMILARITY.  
 FT DISULFID 63 87 BY SIMILARITY.  
 FT DISULFID 79 100 BY SIMILARITY.  
 FT ACT\_SITE 64 65 REACTIVE BOND (BY SIMILARITY).  
 FT DISULFID 125 175 BY SIMILARITY.  
 FT DISULFID 134 158 BY SIMILARITY.  
 FT DISULFID 150 171 BY SIMILARITY.  
 FT ACT\_SITE 135 136 REACTIVE BOND (BY SIMILARITY).  
 FT DISULFID 217 267 BY SIMILARITY.  
 FT DISULFID 226 250 BY SIMILARITY.  
 FT DISULFID 242 263 BY SIMILARITY.  
 FT ACT\_SITE 227 228 REACTIVE BOND (BY SIMILARITY).  
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 195 195 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 256 256 N-LINKED (GLCNAC. .) (POTENTIAL).  
 SQ SEQUENCE 304 AA; 35085 MW; 56E13B3FF16282B0 CRC64;

Query Match 24.9%; Score 236.5; DB 1; Length 304;  
 Best Local Similarity 34.9%; Pred. No. 2e-15;  
 Matches 53; Conservative 24; Mismatches 64; Indels 11; Gaps 4;  
 QY 9 DFCLVSKVGRCRASPRWYNTDSCOLFVYGGCDGNSNNVLTKEECLKKCATVTENA 68  
 Db 123 DFCFLEDPGICRGYTRIFYNNQSKQCFKYGCGLGNNNFETLEECKNTC---EDGL I79  
 QY 69 TG----DLATSRNADSSVPSAPRRQDSHSDMFNYYEYCTANAVTGPCRASFPWWYF 124  
 Db 180 NGFQVDNYGTQLNAVNS--QTP--QSTKVPSPFFPHGPSWCLAPADRGLCRANENRFY 235  
 QY 125 DVERNSCNNFIYGGCRGNKNSYRSEACMLRC 156  
 Db 236 NSVIGKCRPFKYGSGCGGNENNFTSKRECLRAC 267

Search completed: October 18, 2002, 10:34:09  
 Job time : 13 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 18, 2002, 10:33:48 ; Search time 17 Seconds  
(without alignments)  
960.893 Million cell updates/sec

Title: US-09-218-913D-52

Perfect score: 948

Sequence: 1 ADERSIHDFCLVSKVGRG.....ACMLRCFROENPLPLGSK 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_71:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	658	69.4	252	2 JG0185	hepatocyte growth
2	250.5	26.4	1558	2 C89114	protein C37C3.6a [
3	250.5	26.4	2167	2 T34395	hypothetical prote
4	249.5	26.3	352	1 TI00B1	alpha-1-microglobu
5	246.5	26.0	302	1 TI07GK	tissue factor path
6	244.5	25.8	123	2 A29652	inter-alpha-trypsi
7	244.5	25.8	352	1 HCHU	alpha-1-microglobu
8	244	25.7	299	2 I46937	tissue factor path
9	243	25.6	300	2 S12143	lipoprotein-associ
10	242.5	25.6	337	1 TI00B1	alpha-1-microglobu
11	241.5	25.5	125	1 TI00B1	alpha-1-microglobu
12	240	25.3	2225	2 T26063	hypothetical prote
13	239.5	25.3	396	2 S53325	tissue factor path
14	237.5	25.1	349	2 S21089	alpha-1-microglobu
15	236.5	24.9	304	1 JC2264	tissue factor path
16	235.5	24.8	349	2 S35708	alpha-1-microglobu
17	233.5	24.6	304	1 TI07GK	tissue factor path
18	222	23.4	1043	2 T19734	hypothetical prote
19	219	23.1	922	2 T23573	hypothetical prote
20	214.5	22.6	235	2 A54951	tissue factor path
21	210	22.2	765	2 S42880	amyloid precursor
22	209	22.0	1743	2 T26859	hypothetical prote
23	208	21.9	751	2 A49974	beta-amyloid precu
24	200	21.1	763	2 A49321	amyloid beta (A4)
25	200	21.1	1599	2 T16210	hypothetical prote
26	199	21.0	1522	2 H88380	protein T22F7.3 [
27	195	20.6	1391	2 T20406	hypothetical prote
28	193.5	20.4	111	2 S41082	amyloid precursor
29	193	20.4	1474	2 D88550	protein ZC84.6 [im

30	193	20.4	2844	2 S28291	hypothetical prote
31	191	20.1	1416	2 E88550	protein ZC84.1 [im
32	186.5	19.7	747	2 JH0773	Alzheimer's diseas
33	186	19.6	484	4 A32761	hypothetical Alzhe
34	186	19.6	770	1 QRH0A4	Alzheimer's diseas
35	185.5	19.6	1203	2 T21275	hypothetical prote
36	181.5	19.1	355	1 S22181	gamma-1-microglobu
37	178	18.8	1965	2 T33216	hypothetical prote
38	175.5	18.5	76	2 S03607	Alzheimer's diseas
39	174.5	18.4	76	2 S04855	Alzheimer's diseas
40	174.5	18.4	76	2 S06678	Alzheimer's diseas
41	174.5	18.4	100	2 A32282	Alzheimer's diseas
42	174.5	18.4	692	2 T32980	hypothetical prote
43	167	17.6	62	2 S07451	proteinase inhibit
44	164	17.3	838	2 T20125	hypothetical prote
45	163.5	17.2	372	2 JC2556	alpha-1-microglobu

## ALIGNMENTS

### RESULT 1

JG0185

hepatocyte growth factor activator inhibitor type 2 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 11-May-2000

C:Accession: JG0185

R:Ittoh, H.; Kataoka, H.; Hamasuna, R.; Kitamura, N.; Kono, M.

Biochem. Biophys. Res. Commun. 255, 740-746, 1999

A:Title: Hepatocyte growth factor activator inhibitor type 2 lacking the first kunitz

A:Reference number: JG0185; MUID:99160423

A:Accession: JG0185

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-252 <ITO>

A:Cross-references: GB:AF099016

C:Superfamily: animal Kunitz-type proteinase inhibitor homology

F:133-183/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 69.4%; Score 658; DB 2; Length 252;  
Best Local Similarity 68.2%; Pred. No. 9.6e-52;  
Matches 116; Conservative 20; Mismatches 34; Indels 0; Gaps 0;

QY 1 ADERSIHDFCLVSKVGRASMPRWYNTDSCOLFVYGGDGNNSNLYTKKECLKK 60

Db 28 ASRELDVHESCGVSKVVKCRASIPRWYNTDSCOLFVYGGDGNNSNLYTKKECLKK 87

QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNEEYCTANAVTGPCRASFP 120

Db 88 CAGVTENTDDNARNRGADSSVLSVPRKQSAEDLSAEIENEYCVKAVTGPCRAAFP 147

QY 121 RWYFDVERNSCNFIYGGCRGNKNSYSEACMLRCFROENPLPLGSK 170

Db 148 RWYDTEKNKSCIFVYGGCRGNKNSYLSQACMOHCGKQMHPLPLGK 197

### RESULT 2

C89114

protein C37C3.6a [Imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001

C:Accession: C89114

R:Anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bio

A:Reference number: A75000; MUID:99069613; PMID:9851916

A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C-

A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;

A:Accession: C89114

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1558 <STO>

A:Cross-references: GB:chr\_V; PIDN:AAC25867.1; PID:g3294501; GSPDB:GN00023; CESP:C37C







A:Molecule type: protein  
A:Residues: 20-24 <CALZ>  
R:Bourguignon, J.; Diarra-Mehrpour, M.; Sesboue, R.; Frain, M.; Sala-Trepat, J.M.; Ma  
Biochim. Biophys. Res. Commun. 131, 1146-1153, 1985  
A::Title: Human inter-alpha-trypsin-inhibitor: characterization and partial nucleotide  
A:Reference number: I52208; MUID:86025577  
A:Accession: I52208  
A>Status: translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 302-352 <BOU>  
A:CROSS-references: GB:M11562; NID:g186587; PIDN:AAA59194.1; PID:g307077  
R:Wojcik, E.G.C.: van den Berg, M.; van der Linden, I.K.; Poort, S.R.; Cuppers, R.; Be  
Biochem. J. 311, 753-759, 1995  
A::Title: Factor IX Zuthphen: a Cys(18) -> Arg mutation results in formation of a hetero  
A:Reference number: S59509; MUID:96067589  
A:Accession: S59509  
A:Molecule type: protein  
A:Residues: 27-35,'Y','37' <WOJ>  
R:Atmani, F.; Mizon, J.; Khan, S.R.  
Eur. J. Biochem. 236, 984-990, 1996  
A::Title: Identification of uronic-acid-rich proteins as urinary bikunin, the light chain  
A:Reference number: S66434; MUID:96270753  
A:Accession: S66434  
A:Molecule type: protein  
A:Residues: 206-214,'X','216'-230 <ATM2>  
R:Akerstroem, B.; Bratt, T.; Engchild, J.J.  
FEBS Lett. 362, 50-54, 1995  
A::Title: Formation of the alpha(1)-microglobulin chromophore in mammalian and insect  
A:Reference number: S68728; MUID:95212582  
A:Accession: S68728  
A:Molecule type: protein  
A:Residues: 89-100 <AKE>  
R:Jessen, T.E.; Faarvang, K.L.; Ploug, M.  
FEBS Lett. 230, 195-200, 1988  
A::Title: Carbohydrate as covalent crosslink in human inter-alpha-trypsin inhibitor: a  
A:Reference number: S02431; MUID:88167187  
A:Accession: S02431  
A:Molecule type: protein  
A:Residues: 206-214,'X','216'-217 <YES>  
R:Lopez, C.; Grubb, A.; Mendez, E.  
FEBS Lett. 144, 349-353, 1982  
A::Title: Human protein HC displays variability in its carboxyl-terminal amino acid se  
A:Reference number: A91304  
A:Contents: annotation; variant of alpha-1-microglobulin  
A>Note: pooled urine samples contained two forms of this protein, both lacking 57-Lys  
R:Hochstrasser, K.; Schonberger, O.L.; Rossmannith, I.; Wachter, E.  
Hoppe-Seyler's z. Physiol. Chem. 362, 1357-1362, 1981  
A::Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inte  
by affinity chromatography.  
A:Reference number: A91698; MUID:82074265  
A:Contents: annotation; carbohydrate binding sites  
R:Moril, M.; Travis, J.  
Biol. Chem. Hoppe-Seyler 366, 19-21, 1985  
A::Title: The reactive site of human inter-alpha-trypsin inhibitor is in the amino-term  
A:Reference number: A90682; MUID:85225940  
A:Contents: annotation; inhibitory site  
A>Note: in vitro, the first twelve residues of the amino end of the inhibitor appear  
  
C:Comment: Alpha-1-microglobulin and inter-alpha-trypsin inhibitor are proteolyticall  
C:Comment: Alpha-1-microglobulin occurs in many physiological fluids including plasma  
. It contains at least one brown-yellow chromophore.

Query Match      25.8%; Score 244.5; DB 1; Length 352;  
Best Local Similarity    32.4%; Pred. No. 1.6e+14;  
Matches     48; Conservative    14; Mismatches    47; Indels    39; Gaps    1;

QY        9 DCLVSKVRGCRASPRWMYNVTGDSCQLFVVYGCGDGNNNYLTKRECLKKCATVTENA    68

Dbb      229 DSOLGLVSAGPCMGMSRYFYNGTSMACETFFQGCGMCNGNNVFTEKECLQTCTVA--    286

QY      69 TGDLATSRNAADSVSPAPRRQSDSHSSDMFNVEEYCITANAVTGPCRASFPRWFEDVER    128

Ddb      287 -----CNLPYVRGPCRAFIOWAFDAVI    309

**Qy**   **129** NSCNNFIYGGCRGNKNSYSRSEACMLRC   **156**

                |   |||:-||     |-:-||-|  
**Dd**   **310** GKCVLFPPYGCGGNGNKFYSKECREYC   **337**

**RESULT 8**

I46937  
tissue factor pathway inhibitor - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C>Date: 04-Sep-1997 #sequence\_revision 04-Sep-1997 #text\_change 13-Aug-1999  
C:Accession: I46937  
E:Belaouaj, A.; Kuppuswamy, M.N.; Birktoft, J.J.; Bajaj, S.P.  
Thromb. Res. 69, 547-553, 1993  
A>Title: Revised cdna sequence of rabbit tissue factor pathway inhibitor.  
A:Reference number: I46937; UID:93276427  
A:Accession: I46937  
A>Status: preliminary; translated from GB/EMBL/DDBB  
A:Molecule type: mRNA  
A:Residues: 1-299 <BEL>  
C:Cross-references: GB:S61902; NID:g386015; PIDN:AAB26836.1; PID:g386016  
C:Superfamily: tissue factor pathway inhibitor; animal kunitz-type proteinase inhibitor  
F:49-99/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>  
F:120-170/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>  
F:212-262/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>

Query Match              25.7%; Score 244; DB 2; Length 299;  
Best Local Similarity    30.0%; Pred.No.1.5e-14;  
Matches                48; Conservative    23; Mismatches    61; Indels    28; Gaps    2;

**Qy**   **4** ERSIHDFCLVKVVGRCRASMPRWNYVDGSQLFYVGGDGSNNYLTKEECLKKCAT   **63**

      :: |:: | |:: : ||:: :: |:: |:: |:: |:: |:: |:: |:: |:  
**Dd**   **42** QKPHTSFCAKVDDGPCRAYIKRFENLTHQCEFIYGCGEFNRETFESLECKEKCAR   **101**

**Qy**   **64** VTENATGLATSNAADSSVSAPRRQSDHSDSMFNEVEYCTANAVTGPCRASFPFRWY   **123**

                |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |:  
**Dd**   **102** DYPMTWKTLTQKKPD-----FCFLDEDPGICRGVTITRYF   **137**

**Qy**   **124** FDVERNSCNFIFYGCCGRGNKNYSREEACMLRCFRQQENP   **163**

      :: | | | | | | | | | | | | | | | | | | | | | | | | | | | |:  
**Dd**   **138** YNQSKOCERFKYGGCLGNLNFLESLECKNTC----ENP   **173**

**RESULT 9**

S12143  
lipoprotein-associated coagulation inhibitor precursor - rabbit  
N:Alternate names: endothelial cell coagulation inhibitor; endothelial cell tissue factor  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 16-Jul-1999  
C:Accession: S12143; A61373  
R:Wesselschmidt, R.L.; Girard, T.J.; Broze Jr., G.J.  
Nucleic Acids Res. 18, 6440, 1990  
A>Title: CDNA sequence of rabbit lipoprotein-associated coagulation inhibitor.  
A:Reference number: S12143; UID:91057146  
A:Accession: S12143  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-300 <WES>  
C:Cross-references: EMBL:X54708; NID:g1612; PIDN:CAA38515.1; PID:g1613  
E:Colburn, P.; Crabb, J.W.; Buonassisi, V.  
J. Cell. Physiol. 148, 320-326, 1991  
A>Title: Enhanced inhibition of tissue factor by the extended form of an endothelial cel  
A:Reference number: A61373; UID:91349227  
A:Accession: A61373  
A:Molecule type: protein  
A:Residues: 23-33; X\_335-46 <COL>  
C:Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor  
C:Keywords: anticoagulant; glycoprotein  
F:50-100/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>  
F:121-171/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>  
F:213-263/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>

Query Match              25.6%; Score 243; DB 2; Length 300;

A:Molecule type: DNA  
A:Residues: 1-2225 <MUL>  
A:Cross-references: EMBL:292815; PIDN:CAB07294.1; GSPDB:GN00023; CESP:W01F3.3  
A:Experimental source: clone W01F3  
C:Genetics:  
A:Gene: CESP.W01F3.3  
A:Map position: 5  
A:Introns: 33/1; 56/1; 100/1; 142/3; 271/3; 451/1; 525/3; 774/1; 1093/1; 1178/1; 1221/1

Query Match                25.3%    Score 240; DB 2; Length 2225;  
Best Local Similarity    29.3%;    Pred. No. 2.9e-13;  
Matches          46; Conservative    21; Mismatches    58; Indels     32; Gaps      2;

QY    11 CLVSKVVGRCPASPRWWYNVTGSCQLFYGGCDGNSNNYLTKKECLKKC--ATVTENA 68  
      || | | : : : : : : : : : : : : : : : : : : : : : :  
Db    777 CLHPRDNGNCRGVRFWFDDKKNCKNVFTYTGCQGNNGNFASKEECAICHKEPTPSA 836  
      || | | : : : : : : : : : : : : : : : : : : : : : :  
QY    69 TGLDLSRNAADSVSAPRRQDSHSDMFNTYEECTANAVTGPCRASPPRYFDVER 128  
      || | | : : : : : : : : : : : : : : : : : : : : : :  
Db    837 TPD-----FSQVCNSVDVDAECNGVFERFAFDAEA 866  
      || | | : : : : : : : : : : : : : : : : : : : : : :

QY    129 NSCNFFTYGGCGRNKNSYRSEACMLRCFRQENPPL 165  
      || | | | | : : : : : : : : : : : : : : : : : : : : : :  
Db    867 QDCRAFTYGGCGNGNFATMOECSRCSVMAMKKSPV 903  
      || | | | | : : : : : : : : : : : : : : : : : : : : : :

RESULT 13  
S53325  
tissue factor pathway inhibitor - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C>Date: 01-Aug-1995 #sequence\_revision 01-Sep-1995 #text\_change 16-Jul-1999  
C:Accession: S53325  
R:Girard, T.J.; Gallani, D.; Broze Jr., G.J.  
Biochem. J. 303, 923-928, 1994  
A>Title: Complementary DNA sequencing of canine tissue factor pathway inhibitor reveals  
A:Reference number: S53325; MUID:95071310  
A:Accession: S53325  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-396 <GIR>  
C:Superfamily: animal Kunitz-type proteinase inhibitor homology  
C:Keywords: serine proteinase inhibitor  
F:53-103/domain: animal Kunitz-type proteinase inhibitor homology <BP1>  
F:125-175/domain: animal Kunitz-type proteinase inhibitor homology <BP2>  
F:309-359/domain: animal Kunitz-type proteinase inhibitor homology <BP3>

Query Match                25.3%    Score 239.5; DB 2; Length 396;  
Best Local Similarity    29.6%;    Pred. No. 5.2e-14;  
Matches          4; Conservative    24; Mismatches    60; Indels     23; Gaps      1;

QY    5 RSIHDFCLVSXVGRCRASMPRWNYNTDGSCQLFYGGCDGNSNNYLTKKECLKCATV 64  
      || | | : : : : : : : : : : : : : : : : : : : : : :  
Db    47 RLLHSFCALKADNGPCRAMIRNYFNFIHQCEEFYIGCGEGNQNRPFSLBECEKCVRV 106  
      || | | : : : : : : : : : : : : : : : : : : : : : :  
QY    65 TENATGDLTSRNAADSSVSPARQDSHSDMFNVEEYCTANAVTGPCRASPFPWPYF 124  
      || | | : : : : : : : : : : : : : : : : : : : : : :  
Db    107 YPKA-----KTFLEVKLEKPDYCHMNEDSGLCRGFVRTYYI 143  
      || | | : : : : : : : : : : : : : : : : : : : : : :

QY    125 DVERNSCNFFTYGGCGRNKNSYRSEACMLRC 156  
      || | | | | : : : : : : : : : : : : : : : : : : : : : :  
Db    144 NNVSSKCEGFYGGCLGLNLNFETLEQCKNTC 175  
      || | | : : : : : : : : : : : : : : : : : : : : : :

RESULT 14  
S21089  
alpha-1-microglobulin/inter-alpha-trypsin inhibitor light chain precursor - rat  
N:Alternate names: acid-stable proteinase inhibitor; bikunin; trypstatin  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 22-Nov-1993 #sequence\_revision 01-Sep-1995 #text\_change 04-Feb-2000  
C:Accession: S21089; A53056; A25935; A31890; A61633  
R:Lindqvist, A.; Bratt, T.; Alsterlund, M.; Kasteren, W.; Akerstrom, B.  
Biochim. Biophys. Acta 1130, 63-67, 1992  
A>Title: Rat alpha(1)-microglobulin: co-expression in liver with the light chain of

[illegible]



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 18, 2002, 10:33:48 ; Search time 32 Seconds  
(without alignments)  
590.080 Million cell updates/sec

Title: US-09-218-913D-52

Perfect score: 948

Sequence: 1 ADDRESSIHDFCLVSKVGRG.....ACMLRCFRQENPPPLGSK 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_032802.\*

- 1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*
- 2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*
- 3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*
- 4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*
- 5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*
- 6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*
- 7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*
- 8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*
- 9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*
- 10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*
- 11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*
- 12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*
- 13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*
- 14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*
- 15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*
- 16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*
- 17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*
- 18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*
- 19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*
- 20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*
- 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*
- 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	948	100.0	170	18 AAW30041	Human placental bi
2	948	100.0	170	21 AAB14189	Human placental bi
3	948	100.0	170	21 AAB14190	Human placental bi
4	948	100.0	179	18 AAW30053	Human placental bi
5	948	100.0	179	21 AAB14159	Mature human place
6	948	100.0	197	18 AAW30043	Human placental bi
7	948	100.0	197	21 AAB14160	Human placental bi
8	948	100.0	213	18 AAW30042	Human placental bi
9	948	100.0	213	21 AAB14184	Human placental bi
10	948	100.0	213	21 AAB14200	Human placental bi
11	948	100.0	225	18 AAW30046	Human placental bi

12	948	100.0	225	21 AAB14186	Human placental bi
13	948	100.0	225	21 AAB14201	Human placental bi
14	948	100.0	235	18 AAW30060	Human consensus bi
15	948	100.0	235	21 AAB14167	Human placental bi
16	948	100.0	240	18 AAW30045	Human placental bi
17	948	100.0	248	18 AAW30044	Human consensus bi
18	948	100.0	248	21 AAB14183	Human placental bi
19	948	100.0	252	18 AAW30040	Human placental bi
20	948	100.0	252	18 AAW13665	Hepatocyte growth
21	948	100.0	252	19 AAW70286	Human tissue facto
22	948	100.0	252	21 AAB14187	Human placental bi
23	948	100.0	259	21 AAB14207	Human placental bi
24	948	100.0	289	21 AAB43821	Human cancer assoc
25	945	99.7	240	21 AAB14185	Human placental bi
26	945	99.7	252	22 ABB50286	Kunitz type 2 Ser
27	859	90.6	153	18 AAW30051	Human placental bi
28	859	90.6	153	21 AAB14161	Human placental bi
29	819	86.4	146	18 AAW30052	Human placental bi
30	819	86.4	146	21 AAB14188	Human placental bi
31	750	79.1	170	18 AAW30061	Human consensus bi
32	750	79.1	179	21 AAB14168	Human placental bi
33	501	52.8	92	18 AAW30054	Human placental bi
34	501	52.8	92	21 AAB14166	Human placental bi
35	490	51.7	130	21 AAB14169	Human placental bi
36	488	51.5	130	18 AAW30062	EST R35464 protein
37	487	51.4	169	18 AAW30063	EST R74593 protein
38	487	51.4	169	21 AAB14170	Human placental bi
39	337	35.5	58	18 AAW30049	Human placental bi
40	337	35.5	58	21 AAB14164	Human placental bi
41	334	35.2	58	18 AAW30047	Human placental bi
42	334	35.2	58	21 AAB14162	Human placental bi
43	312	32.9	513	18 AAW27368	Hepatocyte growth
44	312	32.9	513	20 AAW92653	Human HAI-1 protei
45	312	32.9	513	21 AAB19553	Human hepatocyte g

## ALIGNMENTS

RESULT 1	AAW30041	standard; Protein; 170 AA.
ID	AAW30041	
XX	AC	
XX	AAW30041;	
DT	20-APR-1998	(first entry)
XX	XX	
DE	Human placental bikunin.	
XX	XX	
KW	Human; placental bikunin; inhibition; trypsin; kallikrein;	
KW	plasma; factor XIIa; treatment; prevention; oedema;	
KW	inflammation; infection; granulomatosis; multiple sclerosis;	
KW	ischaemia; perioperative blood loss; sepsis; shock; fibrosis;	
KW	blood coagulation disease; polytrauma; stroke; haemorrhage;	
KW	gastric cancer; cervical cancer; metastasis; blood loss.	
XX	OS	Homo sapiens.
XX	XX	
PN	WO9733996-A2.	
XX	PD	18-SEP-1997.
XX	PF	10-MAR-1997; 97WO-US03894.
XX	PR	04-OCT-1996; 96US-0725251.
PR	11-MAR-1996;	96US-0013106.
PR	14-JUN-1996;	96US-0019793.
XX	PA	(FARB ) BAYER CORP.
XX	XX	
PI	Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;	
XX	XX	
DR	WPI; 1997-470876/43.	

XX New human placental bikunin - used to inhibit kallikrein, trypsin  
 PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or  
 PT perioperative blood loss  
 XX  
 PS Claim 1: Page 65; 110pp; English.  
 XX  
 CC The present sequence is a human placental bikunin, which  
 CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.  
 CC Bikunin can be used to treat or prevent brain and spinal cord  
 CC oedema, inflammation, infection or granulomatosis, multiple  
 CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,  
 CC fibrosis, blood coagulation diseases, polytrauma, stroke,  
 CC cerebral or subarachnoid haemorrhage and gastric or cervical  
 CC cancer and prevent metastasis. It is particularly useful for  
 CC reducing blood loss during surgery, and can also be used to treat  
 CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,  
 CC influenza and similar viral infections, acute pancreatitis and  
 CC gout, and prevent pre-term labour. It has similar properties to  
 CC aprotinin, but is less highly charged so should be less  
 CC immunogenic and less likely to damage the kidneys. Manipulation  
 CC of the bikunin sequence may allow the inhibitory profile to be  
 CC altered. It also reduces or eliminates the need for whole donor  
 CC blood or blood products during surgery, thereby reducing the risk  
 CC of infection and other adverse side effects, as well as reducing  
 CC the cost of surgery.  
 XX  
 SQ Sequence 170 AA;  
 Query Match 100.0%; Score 948; DB 18; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 4e-89;  
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ADRERSIHDFCLVSKVVGRCRAMPWWYNTDGSQCLFVYGGCDGNSNNYLTKECLKK 60  
 DB 1 ADRERSIHDFCLVSKVVGRCRAMPWWYNTDGSQCLFVYGGCDGNSNNYLTKECLKK 60  
 QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEEYCTANAVTGPCRASFP 120  
 DB 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEEYCTANAVTGPCRASFP 120  
 QY 121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 170  
 DB 121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 170  
 RESULT 2  
 AAB14189  
 ID AAB14189 standard; protein; 170 AA.  
 AC AAB14189;  
 DT 02-FEB-2001 (first entry)  
 XX Human placental bikunin protein # 7.  
 DE  
 DE Human; mucociliary dysfunction; mucus; sputum;  
 KW chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;  
 KW BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin;  
 KW Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200037099-A2.  
 XX  
 XX 29-JUN-2000.  
 XX  
 XX 22-DEC-1999; 99WO-GB04381.  
 XX  
 XX 22-DEC-1998; 98US-0218913.  
 PR 17-NOV-1999; 99US-0441966.  
 XX  
 XX (FARB ) BAYER AG.

XX Hall R, Poll CT, Newton BB, Taylor WJA;  
 XX WPI; 2000-452127/39.  
 XX  
 PT Stimulating mucociliary clearance rate of mucus and sputum in lung  
 PT airways for treating lung diseases such as cystic fibrosis and  
 PT bronchitis involves administering a Kunitz-type serine protease  
 PT inhibitor -  
 XX  
 PS Disclosure; Pages 166-167; 173pp; English.  
 XX  
 CC Mucociliary dysfunction is the inability of ciliated epithelium to clear  
 CC mucus and sputum in lung airways. Mucociliary dysfunction is a serious  
 CC complication of chronic obstructive lung diseases such as Chronic  
 CC Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF).  
 CC In addition, patients suffering from mucociliary dysfunction are  
 CC susceptible to secondary bacterial infections. The present sequence is  
 CC a sequence for human placental bikunin protein. This sequence was  
 CC derived from a human placental cDNA library by PCR-based amplification.  
 CC This protein is a Kunitz-type serine protease inhibitor protein, which  
 CC can stimulate the rate of mucociliary clearance of mucus and sputum in  
 CC lung airways. Therefore, the present protein may be used for treating  
 CC lung diseases such as CF, CB, BE, and chronic sinusitis and glue ear  
 CC which are caused by retention and accumulation of mucus.  
 CC Note: the present sequence is defined as SEQ ID 51 in the sequence  
 CC listing. However, in figure 4C of the specification, SEQ ID 51 is  
 CC clearly shown as a nucleotide sequence. Therefore, the nucleotide  
 CC sequence has been described in AAA70392.  
 XX  
 SQ Sequence 170 AA;  
 Query Match 100.0%; Score 948; DB 21; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 4e-89;  
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ADRERSIHDFCLVSKVVGRCRAMPWWYNTDGSQCLFVYGGCDGNSNNYLTKECLKK 60  
 DB 1 ADRERSIHDFCLVSKVVGRCRAMPWWYNTDGSQCLFVYGGCDGNSNNYLTKECLKK 60  
 QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEEYCTANAVTGPCRASFP 120  
 DB 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEEYCTANAVTGPCRASFP 120  
 QY 121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 170  
 DB 121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 170  
 RESULT 3  
 AAB14190  
 ID AAB14190 standard; protein; 170 AA.  
 AC AAB14190;  
 DT 02-FEB-2001 (first entry)  
 XX Human placental bikunin protein # 8.  
 DE  
 DE Human; mucociliary dysfunction; mucus; sputum;  
 KW chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;  
 KW BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin;  
 KW Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200037099-A2.  
 XX  
 XX 29-JUN-2000.  
 XX  
 XX 22-DEC-1999; 99WO-GB04381.  
 XX  
 XX 22-DEC-1998; 98US-0218913.  
 PR 17-NOV-1999; 99US-0441966.  
 XX  
 XX (FARB ) BAYER AG.



PR 17-NOV-1999; 99US-0441966.  
 XX (FARB ) BAYER AG.  
 XX PI Hall R, Poll CT, Newton BB, Taylor WJA;  
 XX DR WPI; 2000-452127/39.  
 XX  
 XX Stimulating mucociliary clearance rate of mucus and sputum in lung  
 PT airways for treating lung diseases such as cystic fibrosis and  
 PT bronchitis involves administering a Kunitz-type serine protease  
 PT inhibitor  
 XX  
 XX Claim 14; Page 90; 173pp; English.  
 XX  
 XX Mucociliary dysfunction is the inability of ciliated epithelium to clear  
 CC mucus and sputum in lung airways. Mucociliary dysfunction is a serious  
 CC complication of chronic obstructive lung diseases such as Chronic  
 CC Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF).  
 CC In addition, patients suffering from mucociliary dysfunction are  
 CC susceptible to secondary bacterial infections. The present sequence is  
 CC a sequence for human placental bikunin protein. This sequence was derived  
 CC from a human placental cDNA library by PCR-based amplification. This  
 CC protein is a Kunitz-type serine protease inhibitor protein, which can  
 CC stimulate the rate of mucociliary clearance of mucus and sputum in lung  
 CC airways. Therefore, the present protein may be used for treating lung  
 CC diseases such as CF, CB, BE, and chronic sinusitis and glue ear which  
 CC are caused by retention and accumulation of mucus.  
 XX  
 XX Sequence 170 AA;  
 SQ  
 Query Match 100.0%; Score 948; DB 21; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 4e-89;  
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ADERSITHDFCLVSKVVGRCRASPWWYNVTDGSCQLFVYGGDGNNSNLYLKEECLKK 60  
 DB 1 ADERSITHDFCLVSKVVGRCRASPWWYNVTDGSCQLFVYGGDGNNSNLYLKEECLKK 60  
 QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEHSDMFNYYEYCTANAVTGPCRASFP 120  
 DB 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEHSDMFNYYEYCTANAVTGPCRASFP 120  
 QY 121 RWYFDVERNCSNNFIYGGCRGNKNSRSEACMLRCFROQENPPLPLGSK 170  
 DB 121 RWYFDVERNCSNNFIYGGCRGNKNSRSEACMLRCFROQENPPLPLGSK 170  
 RESULT 4  
 AAW30053  
 ID AAW30053 standard; Protein; 179 AA.  
 XX  
 XX AAW30053;  
 XX  
 XX 20-APR-1998 (first entry)  
 XX  
 XX Human placental bikunin.  
 XX  
 XX Human; placental bikunin; inhibition; trypsin; kallikrein;  
 KW plasmin; factor XIIa; treatment; prevention; oedema;  
 KW inflammation; infection; granulomatosis; multiple sclerosis;  
 KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;  
 KW blood coagulation disease; polytrauma; stroke; haemorrhage;  
 KW gastric cancer; cervical cancer; metastasis; blood loss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX M09733996-A2.  
 PN  
 XX 18-SEP-1997.  
 PD  
 XX  
 XX 10-MAR-1997; 97WO-US03894.  
 PF  
 XX

PR 04-OCT-1996; 96US-0725251.  
 PR 11-MAR-1996; 96US-0013106.  
 PR 14-JUN-1996; 96US-0019793.  
 XX (FARB ) BAYER CORP.  
 XX  
 XX Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;  
 XX WPI; 1997-470876/43.  
 XX  
 XX New human placental bikunin - used to inhibit kallikrein, trypsin  
 PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or  
 PT perioperative blood loss  
 XX  
 XX Claim 1; Page 67; 110pp; English.  
 XX  
 XX The present sequence is a human placental bikunin, which  
 CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.  
 CC Bikunin can be used to treat or prevent brain and spinal cord  
 CC oedema, inflammation, infection or granulomatosis, multiple  
 CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,  
 CC fibrosis, blood coagulation diseases, polytrauma, stroke, cerebral  
 CC or subarachnoid haemorrhage and gastric or cervical  
 CC cancer and prevent metastasis. It is particularly useful for  
 CC reducing blood loss during surgery, and can also be used to treat  
 CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,  
 CC influenza and similar viral infections, acute pancreatitis and  
 CC gout, and prevent pre-term labour. It has similar properties to  
 CC aprotinin, but is less highly charged so should be less  
 CC immunogenic and less likely to damage the kidneys. Manipulation  
 CC of the bikunin sequence may allow the inhibitory profile to be  
 CC altered. It also reduces or eliminates the need for whole donor  
 CC blood or blood products during surgery, thereby reducing the risk  
 CC of infection and other adverse side effects, as well as reducing  
 CC the cost of surgery.  
 XX  
 XX Sequence 179 AA;  
 SQ  
 Query Match 100.0%; Score 948; DB 18; Length 179;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-89;  
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ADERSITHDFCLVSKVVGRCRASPWWYNVTDGSCQLFVYGGDGNNSNLYLKEECLKK 60  
 DB 1 ADERSITHDFCLVSKVVGRCRASPWWYNVTDGSCQLFVYGGDGNNSNLYLKEECLKK 60  
 QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEHSDMFNYYEYCTANAVTGPCRASFP 120  
 DB 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEHSDMFNYYEYCTANAVTGPCRASFP 120  
 QY 121 RWYFDVERNCSNNFIYGGCRGNKNSRSEACMLRCFROQENPPLPLGSK 170  
 DB 121 RWYFDVERNCSNNFIYGGCRGNKNSRSEACMLRCFROQENPPLPLGSK 170  
 RESULT 5  
 AAB14159  
 ID AAB14159 standard; protein; 179 AA.  
 XX  
 XX AAB14159;  
 XX  
 XX 02-FEB-2001 (first entry)  
 XX  
 XX Mature human placental bikunin protein.  
 XX  
 XX Human; mucociliary dysfunction; mucus; sputum;  
 KW chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;  
 KW BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin;  
 KW Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.  
 XX  
 XX Homo sapiens.  
 OS  
 XX W0200037099-A2.  
 PN

XX PD 29-JUN-2000.  
XX PF 22-DEC-1999; 99WO-GB04381.  
XX PR 22-DEC-1998; 98US-0218913.  
XX PR 17-NOV-1999; 99US-0441966.  
XX PA (FARB ) BAYER AG.  
XX PI Hall R, Poll CT, Newton BB, Taylor WJA;  
XX WPI; 2000-452127/39.  
XX PT Stimulating mucociliary clearance rate of mucus and sputum in lung  
PT airways for treating lung diseases such as cystic fibrosis and  
PT bronchitis involves administering a Kunitz-type serine protease  
PT inhibitor -  
XX PS Claim 14; Pages 89-90; 173pp; English.  
XX CC Mucociliary dysfunction is the inability of ciliated epithelium to clear  
CC mucus and sputum in lung airways. Mucociliary dysfunction is a serious  
CC complication of chronic obstructive lung diseases such as Chronic  
CC Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF).  
CC In addition, patients suffering from mucociliary dysfunction are  
CC susceptible to secondary bacterial infections. The present sequence is  
CC human placental bikunin. This protein is a Kunitz-type serine protease  
CC inhibitor protein, which can stimulate the rate of mucociliary clearance  
CC of mucus and sputum in lung airways. Therefore, the present protein may  
CC be used for treating lung diseases such as CF, CB, BE, and chronic  
CC sinusitis and glue ear which are caused by retention and accumulation of  
CC mucus. The present sequence is the mature human placental bikunin protein  
CC sequence.  
XX SQ Sequence 179 AA;  
Query Match 100.0%; Score 948; DB 21; Length 179;  
Best Local Similarity 100.0%; Pred. No. 4.2e-89;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ADERSIHDFCLVSKVVGRCRSMRWYNTDGSQQLFVYGGCDGNSNNYLTKKECLKK 60  
DB 1 ADERSIHDFCLVSKVVGRCRSMRWYNTDGSQQLFVYGGCDGNSNNYLTKKECLKK 60  
QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEEYCTANAVTGPCRASFP 120  
DB 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEEYCTANAVTGPCRASFP 120  
QY 121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEACMLRCFRQENPPLPLGSK 170  
DB 121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEACMLRCFRQENPPLPLGSK 170  
RESULT 6  
AAW30043  
ID AAW30043 standard; Protein; 197 AA.  
AC AAW30043;  
XX 20-APR-1998 (first entry)  
XX Human placental bikunin.  
XX Human; placental bikunin; inhibition; trypsin; kallikrein;  
XX plasmin; factor XIIa; treatment; prevention; oedema;  
XX inflammation; infection; granulomatosis; multiple sclerosis;  
XX ischaemia; perioperative blood loss; sepsis; shock; fibrosis;  
XX blood coagulation disease; polytrauma; stroke; haemorrhage;  
XX gastric cancer; cervical cancer; metastasis; blood loss.  
XX Homo sapiens.  
OS  
XX

PN WO9733996-A2.  
XX 18-SEP-1997.  
XX PF 10-MAR-1997; 97WO-US03894.  
XX PR 04-OCT-1996; 96US-0725251.  
XX PR 11-MAR-1996; 96US-0013106.  
XX PR 14-JUN-1996; 96US-0019793.  
XX PA (FARB ) BAYER CORP.  
XX PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;  
XX WPI; 1997-470876/43.  
XX DR New human placental bikunin - used to inhibit kallikrein, trypsin  
XX etc. in treatment of oedema, multiple sclerosis, fibrosis, or  
XX perioperative blood loss  
XX PS Claim 1; Page 65; 110pp; English.  
XX CC The present sequence is a human placental bikunin, which  
CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.  
CC Bikunin can be used to treat or prevent brain and spinal cord  
CC oedema, inflammation, infection or granulomatosis, multiple  
CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,  
CC fibrosis, blood coagulation diseases, polytrauma, stroke, cerebral  
CC or subarachnoid haemorrhage and gastric or cervical  
CC cancer and prevent metastasis. It is particularly useful for  
CC reducing blood loss during surgery, and can also be used to treat  
CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,  
CC influenza and similar viral infections, acute pancreatitis and  
CC gout, and prevent pre-term labour. It has similar properties to  
CC aprotinin, but is less highly charged so should be less  
CC immunogenic and less likely to damage the kidneys. Manipulation  
CC of the bikunin sequence may allow the inhibitory profile to be  
CC altered. It also reduces or eliminates the need for whole donor  
CC blood or blood products during surgery, thereby reducing the risk  
CC of infection and other adverse side effects, as well as reducing  
CC the cost of surgery.  
XX SQ Sequence 197 AA;  
Query Match 100.0%; Score 948; DB 18; Length 197;  
Best Local Similarity 100.0%; Pred. No. 4.8e-89;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ADERSIHDFCLVSKVVGRCRSMRWYNTDGSQQLFVYGGCDGNSNNYLTKKECLKK 60  
DB 19 ADERSIHDFCLVSKVVGRCRSMRWYNTDGSQQLFVYGGCDGNSNNYLTKKECLKK 78  
QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEEYCTANAVTGPCRASFP 120  
DB 79 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEEYCTANAVTGPCRASFP 138  
QY 121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEACMLRCFRQENPPLPLGSK 170  
DB 139 RWYFDVERNSCNNFIYGGCRGNKNSYRSEACMLRCFRQENPPLPLGSK 188  
RESULT 7  
AAB14160  
ID AAB14160 standard; protein; 197 AA.  
AC AAB14160;  
XX 02-FEB-2001 (first entry)  
XX Human placental bikunin mature protein and signal peptide.  
XX Human; mucociliary dysfunction; mucus; sputum;  
XX chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;  
KW

KW BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin;  
 KW Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.  
 XX  
 XX  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Peptide 1..18  
 FT /label= Signal\_peptide  
 FT Protein 19..197  
 FT /label= Mature\_protein  
 XX  
 XX WO200037099-A2.  
 XX  
 XX 29-JUN-2000.  
 PD  
 XX  
 XX 22-DEC-1999; 99WO-GB04381.  
 XX  
 XX 22-DEC-1998; 98US-0218913.  
 PR 17-NOV-1999; 99US-0441966.  
 XX  
 XX (FARB ) BAYER AG.  
 PA  
 XX Hall R, Poll CT, Newton BB, Taylor WJA;  
 PI  
 XX WPI; 2000-452127/39.  
 DR  
 XX  
 XX Stimulating mucociliary clearance rate of mucus and sputum in lung  
 PT airways for treating lung diseases such as cystic fibrosis and  
 PT bronchitis involves administering a Kunitz-type serine protease  
 PT inhibitor -  
 XX  
 XX Claim 13; Page 88; 173pp; English.  
 PS  
 XX Mucociliary dysfunction is the inability of ciliated epithelium to clear  
 CC mucus and sputum in lung airways. Mucociliary dysfunction is a serious  
 CC complication of chronic obstructive lung diseases such as Chronic  
 CC Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF).  
 CC In addition, patients suffering from mucociliary dysfunction are  
 CC susceptible to secondary bacterial infections. The present sequence is  
 CC human placental bikunin. This protein is a Kunitz-type serine protease  
 CC inhibitor protein, which can stimulate the rate of mucociliary clearance  
 CC of mucus and sputum in lung airways. Therefore, the present protein may  
 CC be used for treating lung diseases such as CF, CB, BE, and chronic  
 CC sinusitis and glue ear which are caused by retention and accumulation of  
 CC mucus. The present sequence is the full-length human placental bikunin  
 CC protein sequence.  
 XX  
 XX Sequence 197 AA;  
 SQ  
 Query Match 100.0%; Score 948; DB 21; Length 197;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-89;  
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ADERSIHDFCLVSKVVGRCRSMRPWWNVTDGSQLFVYGGCDGNSNNYLTKECLKK 60  
 DB 19 ADERSIHDFCLVSKVVGRCRSMRPWWNVTDGSQLFVYGGCDGNSNNYLTKECLKK 78  
 QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEEYCTANAVTGPCRASFP 120  
 DB 79 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEEYCTANAVTGPCRASFP 138  
 QY 121 RWFYDVERNSCNFIYGGCRGNKNSYRSEACMLRCFRQOENPPLPLGSK 170  
 DB 139 RWFYDVERNSCNFIYGGCRGNKNSYRSEACMLRCFRQOENPPLPLGSK 188  
 RESULT 8  
 AAW30042  
 ID AAW30042 standard; Protein; 213 AA.  
 XX  
 AC AAW30042;  
 XX  
 DT 20-APR-1998 (first entry)

XX DE Human placental bikunin.  
 XX  
 KW Human; placental bikunin; inhibition; trypsin; kallikrein;  
 KW plasmin; factor XIIa; treatment; prevention; oedema;  
 KW inflammation; infection; granulomatosis; multiple sclerosis;  
 KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;  
 KW blood coagulation disease; polytrauma; stroke; haemorrhage;  
 KW gastric cancer; cervical cancer; metastasis; blood loss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO9733996-A2.  
 XX  
 XX 18-SEP-1997.  
 PD  
 XX  
 XX 10-MAR-1997; 97WO-US03894.  
 PF  
 XX 04-OCT-1996; 96US-0725251.  
 PR 11-MAR-1996; 96US-0013106.  
 PR 14-JUN-1996; 96US-0019793.  
 XX  
 XX (FARB ) BAYER CORP.  
 PA  
 XX  
 XX Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;  
 PI  
 XX WPI; 1997-470876/43.  
 DR  
 XX New human placental bikunin - used to inhibit kallikrein, trypsin  
 PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or  
 PT perioperative blood loss  
 PT  
 XX Claim 1; Page 65; 110pp; English.  
 PS  
 XX The present sequence is a human placental bikunin, which  
 CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.  
 CC Bikunin can be used to treat or prevent brain and spinal cord  
 CC oedema, inflammation, infection or granulomatosis, multiple  
 CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,  
 CC fibrosis, blood coagulation diseases, polytrauma, stroke,  
 CC cerebral or subarachnoid haemorrhage and gastric or cervical  
 CC cancer and prevent metastasis. It is particularly useful for  
 CC reducing blood loss during surgery, and can also be used to treat  
 CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,  
 CC influenza and similar viral infections, acute pancreatitis and  
 CC gout, and prevent pre-term labour. It has similar properties to  
 CC aprotinin, but is less highly charged so should be less  
 CC immunogenic and less likely to damage the kidneys. Manipulation  
 CC of the bikunin sequence may allow the inhibitory profile to be  
 CC altered. It also reduces or eliminates the need for whole donor  
 CC blood or blood products during surgery, thereby reducing the risk  
 CC of infection and other adverse side effects, as well as reducing  
 CC the cost of surgery.  
 XX  
 XX Sequence 213 AA;  
 SQ  
 Query Match 100.0%; Score 948; DB 18; Length 213;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-89;  
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ADERSIHDFCLVSKVVGRCRSMRPWWNVTDGSQLFVYGGCDGNSNNYLTKECLKK 60  
 DB 1 ADERSIHDFCLVSKVVGRCRSMRPWWNVTDGSQLFVYGGCDGNSNNYLTKECLKK 60  
 QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEEYCTANAVTGPCRASFP 120  
 DB 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEEYCTANAVTGPCRASFP 120  
 QY 121 RWFYDVERNSCNFIYGGCRGNKNSYRSEACMLRCFRQOENPPLPLGSK 170  
 DB 121 RWFYDVERNSCNFIYGGCRGNKNSYRSEACMLRCFRQOENPPLPLGSK 170

RESULT 9  
AAB14184  
ID AAB14184 standard; protein; 213 AA.  
XX AC AAB14184;  
XX DT 02-FEB-2001 (first entry)  
XX DE Human placental bikunin protein # 2.  
XX KW Human; mucociliary dysfunction; mucus; sputum;  
XX KW chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;  
XX KW BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin;  
XX KW Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.  
XX OS Homo sapiens.  
XX PN WO200037099-A2.  
XX PD 29-JUN-2000.  
XX PF 22-DEC-1999; 99WO-GB04381.  
XX PR 22-DEC-1998; 98US-0218913.  
XX PR 17-NOV-1999; 99US-0441966.  
XX PA (FARB ) BAYER AG.  
XX PI Hall R, Poll CT, Newton BB, Taylor WJA;  
XX DR WPI; 2000-452127/39.  
XX PT Stimulating mucociliary clearance rate of mucus and sputum in lung  
XX PT airways for treating lung diseases such as cystic fibrosis and  
XX PT bronchitis involves administering a Kunitz-type serine protease  
XX PT inhibitor  
XX PS Disclosure; Page 162; 173pp; English.  
XX CC Mucociliary dysfunction is the inability of ciliated epithelium to clear  
XX CC mucus and sputum in lung airways. Mucociliary dysfunction is a serious  
XX CC complication of chronic obstructive lung diseases such as Chronic  
XX CC Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF).  
XX CC In addition, patients suffering from mucociliary dysfunction are  
XX CC susceptible to secondary bacterial infections. The present sequence is a  
XX CC fragment of human placental bikunin. Human placental bikunin is a  
XX CC Kunitz-type serine protease inhibitor protein, which can stimulate the  
XX CC rate of mucociliary clearance of mucus and sputum in lung airways.  
XX CC Therefore, the present protein fragment may be used for treating lung  
XX CC diseases such as CF, CB, BE, and chronic sinusitis and glue ear which  
XX CC are caused by retention and accumulation of mucus.  
XX CC Note: the present sequence is defined as SEQ ID 46 in the sequence  
XX CC listing. However, in figure 4E of the specification, SEQ ID 46 is  
XX CC clearly shown as a nucleotide sequence. Therefore, the nucleotide  
XX CC sequence has been described in AAA70393.  
XX SQ Sequence 213 AA;  
Query Match 100.0%; Score 948; DB 21; Length 213;  
Best Local Similarity 100.0%; Pred. No. 5.3e-89;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ADERSIHDFCLVSKVVGRCRAMPWWYNVTDGSCQLFVYGGCDGNSNNYLTKECLKK 60  
Db 1 ADERSIHDFCLVSKVVGRCRAMPWWYNVTDGSCQLFVYGGCDGNSNNYLTKECLKK 60  
QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNFEYCTANAVTGPCRASFP 120  
Db 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNFEYCTANAVTGPCRASFP 120  
QY 121 RWFYDVERNSCNFFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 170  
Db 121 RWFYDVERNSCNFFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 170

RESULT 10  
AAB14200  
ID AAB14200 standard; protein; 213 AA.  
XX AC AAB14200;  
XX DT 02-FEB-2001 (first entry)  
XX DE Human placental bikunin protein fragment # 15.  
XX KW Human; mucociliary dysfunction; mucus; sputum;  
XX KW chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;  
XX KW BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin;  
XX KW Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.  
XX OS Homo sapiens.  
XX PN WO200037099-A2.  
XX PD 29-JUN-2000.  
XX PF 22-DEC-1999; 99WO-GB04381.  
XX PR 22-DEC-1998; 98US-0218913.  
XX PR 17-NOV-1999; 99US-0441966.  
XX PA (FARB ) BAYER AG.  
XX PI Hall R, Poll CT, Newton BB, Taylor WJA;  
XX DR WPI; 2000-452127/39.  
XX PT Stimulating mucociliary clearance rate of mucus and sputum in lung  
XX PT airways for treating lung diseases such as cystic fibrosis and  
XX PT bronchitis involves administering a Kunitz-type serine protease  
XX PT inhibitor  
XX PS Claim 13; Page 88; 173pp; English.  
XX CC Mucociliary dysfunction is the inability of ciliated epithelium to clear  
XX CC mucus and sputum in lung airways. Mucociliary dysfunction is a serious  
XX CC complication of chronic obstructive lung diseases such as Chronic  
XX CC Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF).  
XX CC In addition, patients suffering from mucociliary dysfunction are  
XX CC susceptible to secondary bacterial infections. The present sequence is a  
XX CC fragment of human placental bikunin. Human placental bikunin is a  
XX CC Kunitz-type serine protease inhibitor protein, which can stimulate the  
XX CC rate of mucociliary clearance of mucus and sputum in lung airways.  
XX CC Therefore, the present protein fragment may be used for treating lung  
XX CC diseases such as CF, CB, BE, and chronic sinusitis and glue ear which are  
XX CC caused by retention and accumulation of mucus.  
XX SQ Sequence 213 AA;  
Query Match 100.0%; Score 948; DB 21; Length 213;  
Best Local Similarity 100.0%; Pred. No. 5.3e-89;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ADERSIHDFCLVSKVVGRCRAMPWWYNVTDGSCQLFVYGGCDGNSNNYLTKECLKK 60  
Db 1 ADERSIHDFCLVSKVVGRCRAMPWWYNVTDGSCQLFVYGGCDGNSNNYLTKECLKK 60  
QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNFEYCTANAVTGPCRASFP 120  
Db 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNFEYCTANAVTGPCRASFP 120  
QY 121 RWFYDVERNSCNFFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 170  
Db 121 RWFYDVERNSCNFFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 170

RESULT 11  
AAW30046  
ID AAW30046 standard; Protein; 225 AA.  
XX  
AC AAW30046;  
XX  
DT 20-APR-1998 (first entry)  
XX  
DE Human placental bikunin.  
XX  
KW Human; placental bikunin; inhibition; trypsin; kallikrein;  
KW plasmin; factor XIIa; treatment; prevention; oedema;  
KW inflammation; infection; granulomatosis; multiple sclerosis;  
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;  
KW blood coagulation disease; polytrauma; stroke; haemorrhage;  
KW gastric cancer; cervical cancer; metastasis; blood loss.  
XX  
OS Homo sapiens.  
XX  
PN WO9733996-A2.  
XX  
PD 18-SEP-1997.  
XX  
PF 10-MAR-1997; 97WO-US03894.  
XX  
PR 04-OCT-1996; 96US-0725251.  
PR 11-MAR-1996; 96US-0013106.  
PR 14-JUN-1996; 96US-0019793.  
XX  
PA (FARB ) BAYER CORP.  
XX  
PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;  
XX  
DR WPI; 1997-470876/43.  
XX  
PT New human placental bikunin - used to inhibit kallikrein, trypsin  
PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or  
PT perioperative blood loss  
XX  
PS Claim 1; Page 66; 110pp; English.  
XX  
CC The present sequence is a human placental bikunin, which  
CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.  
CC Bikunin can be used to treat or prevent brain and spinal cord  
CC oedema, inflammation, infection or granulomatosis, multiple  
CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,  
CC fibrosis, blood coagulation diseases, polytrauma, stroke,  
CC cerebral or subarachnoid haemorrhage and gastric or cervical  
CC cancer and prevent metastasis. It is particularly useful for  
CC reducing blood loss during surgery, and can also be used to treat  
CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,  
CC influenza and similar viral infections, acute pancreatitis and  
CC gout, and prevent pre-term labour. It has similar properties to  
CC aprotinin, but is less highly charged so should be less  
CC immunogenic and less likely to damage the kidneys. Manipulation  
CC of the bikunin sequence may allow the inhibitory profile to be  
CC altered. It also reduces or eliminates the need for whole donor  
CC blood or blood products during surgery, thereby reducing the risk  
CC of infection and other adverse side effects, as well as reducing  
CC the cost of surgery.  
XX  
SQ Sequence 225 AA;

Query Match 100.0%; Score 948; DB 18; Length 225;  
Best Local Similarity 100.0%; Pred. No. 5.7e-89;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADERSIHDFCLVSKVVGRCRAMPWWNVTDGSCQLFVYGGCDGNSNNYLTKECLKK 60  
|||||  
DB 1 ADERSIHDFCLVSKVVGRCRAMPWWNVTDGSCQLFVYGGCDGNSNNYLTKECLKK 60  
|||||

QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSDMFNEYCYTANAVTGPCRASFP 120  
|||||

DB 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSDMFNEYCYTANAVTGPCRASFP 120  
QY 121 RWFYDVERNSCNFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 170  
|||||  
DB 121 RWFYDVERNSCNFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 170  
|||||

RESULT 12  
AAB14186  
ID AAB14186 standard; protein; 225 AA.  
XX  
AC AAB14186;  
XX  
DT 02-FEB-2001 (first entry)  
XX  
DE Human placental bikunin protein # 4.  
XX  
KW Human; mucociliary dysfunction; mucus; sputum;  
KW chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;  
KW BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin;  
KW Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.  
XX  
OS Homo sapiens.  
XX  
PN WO200037099-A2.  
XX  
PD 29-JUN-2000.  
XX  
PF 22-DEC-1999; 99WO-GB04381.  
PR 22-DEC-1998; 98US-0218913.  
PR 17-NOV-1999; 99US-0441966.  
XX  
PA (FARB ) BAYER AG.  
XX  
PI Hall R, Poll CT, Newton BB, Taylor WJA;  
XX  
DR WPI; 2000-452127/39.  
XX  
PT Stimulating mucociliary clearance rate of mucus and sputum in lung  
PT airways for treating lung diseases such as cystic fibrosis and  
PT bronchitis involves administering a Kunitz-type serine protease  
PT inhibitor  
XX  
PS Disclosure; Page 164; 173pp; English.  
XX  
CC Mucociliary dysfunction is the inability of ciliated epithelium to clear  
CC mucus and sputum in lung airways. Mucociliary dysfunction is a serious  
CC complication of chronic obstructive lung diseases such as Chronic  
CC Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF).  
CC In addition, patients suffering from mucociliary dysfunction are  
CC susceptible to secondary bacterial infections. The present sequence is a  
CC fragment of human placental bikunin. Human placental bikunin is a  
CC Kunitz-type serine protease inhibitor protein, which can stimulate the  
CC rate of mucociliary clearance of mucus and sputum in lung airways.  
CC Therefore, the present protein fragment may be used for treating lung  
CC diseases such as CF, CB, BE, and chronic sinusitis and glue ear which  
CC are caused by retention and accumulation of mucus.  
CC Note: the present sequence is defined as SEQ ID 48 in the sequence  
CC listing. However, in figure 4F of the specification, SEQ ID 48 is  
CC clearly shown as a nucleotide sequence. Therefore, the nucleotide  
CC sequence has been described in AAA70406.  
XX  
SQ Sequence 225 AA;

Query Match 100.0%; Score 948; DB 21; Length 225;  
Best Local Similarity 100.0%; Pred. No. 5.7e-89;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADERSIHDFCLVSKVVGRCRAMPWWNVTDGSCQLFVYGGCDGNSNNYLTKECLKK 60  
|||||  
DB 1 ADERSIHDFCLVSKVVGRCRAMPWWNVTDGSCQLFVYGGCDGNSNNYLTKECLKK 60  
|||||

QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEEYCTANAVTGPCRASEP 120  
|||||  
Db 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEEYCTANAVTGPCRASEP 120  
|||||  
QY 121 RWFDVERNSCNFFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 170  
|||||  
Db 121 RWFDVERNSCNFFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 170  
|||||

RESULT 13  
AAB14201  
ID AAB14201 standard; protein; 225 AA.  
XX  
AC AAB14201;  
XX  
DT 02-FEB-2001 (first entry)  
XX  
DE Human placental bikunin protein fragment # 16.  
XX  
KW Human; mucociliary dysfunction; mucus; sputum;  
KW chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;  
KW BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin;  
KW Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.  
XX  
OS Homo sapiens.  
XX  
PN W0200037099-A2.  
XX  
PD 29-JUN-2000.  
XX  
PF 22-DEC-1999; 99WO-GB04381.  
XX  
PR 22-DEC-1998; 98US-0218913.  
PR 17-NOV-1999; 99US-0441966.  
XX  
PA (FARB ) BAYER AG.  
XX  
PI Hall R, Poll CT, Newton BB, Taylor WJA;  
XX  
PD WPI; 2000-452127/39.  
XX  
PF Stimulating mucociliary clearance rate of mucus and sputum in lung  
PT airways for treating lung diseases such as cystic fibrosis and  
PT bronchitis involves administering a Kunitz-type serine protease  
PT inhibitor  
XX  
PS Claim 13; Pages 88-89; 173pp; English.  
XX  
CC Mucociliary dysfunction is the inability of ciliated epithelium to clear  
CC mucus and sputum in lung airways. Mucociliary dysfunction is a serious  
CC complication of chronic obstructive lung diseases such as Chronic  
CC Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF).  
CC In addition, patients suffering from mucociliary dysfunction are  
CC susceptible to secondary bacterial infections. The present sequence is a  
CC fragment of human placental bikunin. Human placental bikunin is a  
CC Kunitz-type serine protease inhibitor protein, which can stimulate the  
CC rate of mucociliary clearance of mucus and sputum in lung airways.  
CC Therefore, the present protein fragment may be used for treating lung  
CC diseases such as CF, CB, BE, and chronic sinusitis and glue ear which are  
CC caused by retention and accumulation of mucus.  
XX  
SQ Sequence 225 AA;  
Query Match 100.0%; Score 948; DB 21; Length 225;  
Best Local Similarity 100.0%; Pred. No. 5.7e-89;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADERSIHDFCLVSKVGRASMPRWYNVTGDSQQLFVYGGCDGNSNNYLTKECLKK 60  
|||||  
Db 1 ADERSIHDFCLVSKVGRASMPRWYNVTGDSQQLFVYGGCDGNSNNYLTKECLKK 60  
|||||

QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEEYCTANAVTGPCRASEP 120  
|||||

Db 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEEYCTANAVTGPCRASEP 120  
|||||  
QY 121 RWFDVERNSCNFFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 170  
|||||  
Db 121 RWFDVERNSCNFFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 170  
|||||

RESULT 14  
AAW30060  
ID AAW30060 standard; Protein; 235 AA.  
XX  
AC AAW30060;  
XX  
DT 20-APR-1998 (first entry)  
XX  
DE Human consensus bikunin.  
XX  
KW Human; consensus bikunin; inhibition; trypsin; kallikrein;  
KW plasmin; factor XIIa; treatment; prevention; oedema;  
KW inflammation; infection; granulomatosis; multiple sclerosis;  
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;  
KW blood coagulation disease; polytrauma; stroke; haemorrhage;  
KW gastric cancer; cervical cancer; metastasis; blood loss.  
XX  
OS Homo sapiens.  
XX  
PN Key Location/Qualifiers  
FT Misc-difference 198 /note= "encoded by TGA"  
FT Misc-difference 201 /note= "encoded by TGA"  
FT Misc-difference 226 /note= "encoded by GAN"  
FT Misc-difference 233 /note= "encoded by TGA"  
XX  
PN W09733996-A2.  
XX  
PD 18-SEP-1997.  
XX  
PF 10-MAR-1997; 97WO-US03894.  
XX  
PR 04-OCT-1996; 96US-0725251.  
PR 11-MAR-1996; 96US-0013106.  
PR 14-JUN-1996; 96US-0019793.  
XX  
PA (FARB ) BAYER CORP.  
XX  
PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;  
XX  
PD WPI; 1997-470876/43.  
DR N-PSDB; AAT90732.  
XX  
PT New human placental bikunin - used to inhibit kallikrein, trypsin  
PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or  
PT perioperative blood loss  
XX  
PS Disclosure; Fig 3; 110pp; English.  
XX  
CC The present sequence is a consensus human bikunin, which  
CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.  
CC Bikunin can be used to treat or prevent brain and spinal cord  
CC oedema, inflammation, infection or granulomatosis, multiple  
CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,  
CC fibrosis, blood coagulation diseases, polytrauma, stroke,  
CC cerebral or subarachnoid haemorrhage and gastric or cervical  
CC cancer and prevent metastasis. It is particularly useful for  
CC reducing blood loss during surgery, and can also be used to treat  
CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,  
CC influenza and similar viral infections, acute pancreatitis and  
CC gout, and prevent pre-term labour. It has similar properties to  
CC aprotinin, but is less highly charged so should be less  
CC immunogenic and less likely to damage the kidneys. Manipulation

CC of the bikunin sequence may allow the inhibitory profile to be  
 CC altered. It also reduces or eliminates the need for whole donor  
 CC blood or blood products during surgery, thereby reducing the risk  
 CC of infection and other adverse side effects, as well as reducing  
 CC the cost of surgery.

XX  
 SQ Sequence 235 AA;

Query Match 100.0%; Score 948; DB 18; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 6e-89; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADERSIHDFCLVSKVVGRCRASMPRWYNTDGSQCLFVYGGCDGNSNNYLTKEECLKK 60  
 DB 19 ADERSIHDFCLVSKVVGRCRASMPRWYNTDGSQCLFVYGGCDGNSNNYLTKEECLKK 78

QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEEYCTANAVTGPCRASFP 120  
 DB 79 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEEYCTANAVTGPCRASFP 138

QY 121 RWYFDVERNSCNNFIYGGCGRNKNSYRSEACMLRCFROQENPPLPLGSK 170  
 DB 139 RWYFDVERNSCNNFIYGGCGRNKNSYRSEACMLRCFROQENPPLPLGSK 188

RESULT 15  
 AAB14167  
 ID AAB14167 standard; Protein; 235 AA.  
 XX AAB14167;  
 AC AAB14167;  
 DT 02-FEB-2001 (first entry)  
 XX Human placental bikunin protein fragment # 7.  
 DE Human;  
 XX Human; mucociliary dysfunction; mucus; sputum;  
 KW chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;  
 KW BE; asthma; cystic fibrosis; CF; Bacterial infection; placental bikunin;  
 KW Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.  
 XX Homo sapiens.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 198  
 FT /label= unknown  
 FT /note= "Encoded by TGA"  
 FT Misc-difference 201  
 FT /label= unknown  
 FT /note= "Encoded by TGA"  
 FT Misc-difference 207  
 FT /label= "Encoded by GCN"  
 FT /note= "Encoded by GCN"  
 FT Misc-difference 226  
 FT /label= unknown  
 FT /note= "Encoded by GAN"  
 FT Misc-difference 233  
 FT /label= unknown  
 FT /note= "Encoded by TGA"  
 XX  
 PN WO200037099-A2.  
 XX  
 XX 29-JUN-2000.  
 XX  
 XX 22-DEC-1999; 99WO-GB04381.  
 XX  
 XX 22-DEC-1998; 98US-0218913.  
 PR  
 PR 17-NOV-1999; 99US-0441966.  
 XX  
 XX (FARB ) BAYER AG.  
 PA  
 XX Hall R, Poll CT, Newton BB, Taylor WJA;  
 PI  
 XX WPI; 2000-452127/39.  
 DR N-PSDB; AAA70364.

XX Stimulating mucociliary clearance rate of mucus and sputum in lung  
 PT airways for treating lung diseases such as cystic fibrosis and  
 PT bronchitis involves administering a Kunitz-type serine protease  
 PT inhibitor

XX  
 PS Disclosure; Fig 3; 173pp; English.

XX  
 CC Mucociliary dysfunction is the inability of ciliated epithelium to clear  
 CC mucus and sputum in lung airways. Mucociliary dysfunction is a serious  
 CC complication of chronic obstructive lung diseases such as Chronic  
 CC Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF).  
 CC In addition, patients suffering from mucociliary dysfunction are  
 CC susceptible to secondary bacterial infections. The present sequence is a  
 CC human placental bikunin protein fragment. This protein is a Kunitz-type  
 CC serine protease inhibitor protein, which can stimulate the rate of  
 CC mucociliary clearance of mucus and sputum in lung airways. Therefore, the  
 CC present sequence may be used for treating lung diseases such as CF, CB,  
 CC BE, and chronic sinusitis and glue ear which are caused by retention and  
 CC accumulation of mucus.

XX  
 SQ Sequence 235 AA;

Query Match 100.0%; Score 948; DB 21; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 6e-89;  
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADERSIHDFCLVSKVVGRCRASMPRWYNTDGSQCLFVYGGCDGNSNNYLTKEECLKK 60  
 DB 19 ADERSIHDFCLVSKVVGRCRASMPRWYNTDGSQCLFVYGGCDGNSNNYLTKEECLKK 78

QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEEYCTANAVTGPCRASFP 120  
 DB 79 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEEYCTANAVTGPCRASFP 138

QY 121 RWYFDVERNSCNNFIYGGCGRNKNSYRSEACMLRCFROQENPPLPLGSK 170  
 DB 139 RWYFDVERNSCNNFIYGGCGRNKNSYRSEACMLRCFROQENPPLPLGSK 188

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